

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 7, 2006, 08:38:47 ; Search time 938.432 Seconds

(without alignments)
1090.310 Million cell updates/sec

Title: US-10-659-980A-5

Perfect score: 18
Sequence: 1 cccccctctctgcatc 18

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 1641224

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	18	100.0	18	6	CQ796912 Sequence
2	18	100.0	18	6	CS089158 Sequence
3	18	100.0	18	6	AX316096 Sequence
4	16.4	91.1	18	6	CS089171 Sequence
5	16.4	91.1	18	6	AX316109 Sequence
6	14.4	80.0	30	6	AR083535 Sequence
7	13.8	76.7	18	6	CQ796928 Sequence
8	13.8	76.7	28	6	AX191455 Sequence
9	12.8	71.1	17	6	AR568743 Sequence
10	12.4	68.9	17	6	BD254227 Sequence
11	12.4	68.9	20	6	BD254228 Sequence
12	12.4	68.9	20	6	CO801520 Sequence
13	12.4	68.9	20	6	AR311956 Sequence
14	12.2	67.8	17	6	BD197714 Method an
15	12.2	67.8	23	6	II2779 Sequence 77
16	12.2	67.8	23	6	AX355960 Sequence
17	12.2	67.8	26	6	AX922612 Sequence
18	12.2	67.8	27	6	CS050694 Sequence

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C	23	12	66.7	17	6	AX733930	AX733930 Sequence
C	24	12	66.7	17	6	AX760134	AX760134 Sequence
C	25	12	66.7	18	6	CQ796913	CQ796913 Sequence
C	26	12	66.7	18	6	CS089159	CS089159 Sequence
C	27	12	66.7	18	6	AX316097	AX316097 Sequence
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C	29	12	66.7	18	6	AX112294	AX112294 Sequence
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C	31	12	66.7	20	6	AX298879	AX298879 Sequence
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C	34	11.8	65.6	20	6	AR444884	AR444884 Sequence
C	35	11.8	65.6	21	11	CS000256	CS000256 Sequence
C	36	11.8	65.6	23	6	CO888258	CO888258 Sequence
C	37	11.8	65.6	24	6	AR054071	AR054071 Sequence
C	38	11.8	65.6	24	6	AR127460	AR127460 Sequence
C	39	11.8	65.6	25	6	AR239155	AR239155 Sequence
C	40	11.8	65.6	25	6	AX278957	AX278957 Sequence
C	41	11.8	65.6	26	6	AX556664	AX556664 Sequence
C	42	11.6	64.4	18	6	A00428	A00428 Nucleotide
C	43	11.6	64.4	23	6	II2780	II2780 Sequence 78
C	44	11.6	64.4	24	6	CQ778009	CQ778009 Sequence
C	45	11.6	64.4	25	6	CO627125	CO627125 Sequence

ALIGNMENTS

RESULT 1	CQ796912	18 bp	DNA	linear	PAT 19-APR-2004
LOCUS	CQ796912	Sequence 5 from Patent WO2004026772.			
DEFINITION	CQ796912				
ACCESSION	CQ796912.1	GI:46408538			
VERSION	CQ796912.1	GI:46408538			
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
FEATURES					
source					
ORIGIN					
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QY	1	CCCCCCTTCTCGATAC	18		
Db	1	CCCCCCTTCTCGATAC	18		
RESULT 2	CS089158	18 bp	DNA	linear	PAT 25-MAY-2005
LOCUS	CS089158	Sequence 5 from Patent EP1502948.			
DEFINITION	CS089158				
ACCESSION	CS089158.1	GI:66714442			
VERSION	CS089158.1	GI:66714442			
KEYWORDS					
SOURCE					
synthetic construct					

ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Hovanec, T.A. and Burrell, P.C.
TITLE Ammonia-oxidizing bacteria
JOURNAL Patent: EP 1502948-A 5 02-FEB-2005;
Aguarita Inc. (US)
FEATURES Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Description of Artificial Sequence: Probe"

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Best Local Similarity 100.0%; Pred. No. 67;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCCCTCTTGATAC 18
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Db 1 CCCCCCTCTTGATAC 18

RESULT 3
AX316096 18 bp DNA linear PAT 14-DEC-2001
LOCUS AX316096
DEFINITION Sequence 5 from Patent WO0190312.
ACCESSION AX316096
VERSION AX316096.1 GI:17899287
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Hovanec, T.A. and Burrell, P.C.
TITLE Ammonia-oxidizing bacteria
JOURNAL Patent: WO 0190312-A 5 29-NOV-2001;
AQUARIA, INC. (US)
FEATURES Location/Qualifiers
source 1..18
"/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Probe"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 67;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCCCTCTTGATAC 18
1 CCCCCCTCTTGATAC 18

Db 1 CCCCCCTCTTGATAC 18

RESULT 4
CS089171 18 bp DNA linear PAT 25-MAY-2005
LOCUS CS089171
DEFINITION Sequence 18 from Patent EP1502948.
ACCESSION CS089171
VERSION CS089171.1 GI:66714455
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Hovanec, T.A. and Burrell, P.C.
TITLE Ammonia-oxidizing bacteria
JOURNAL Patent: EP 1502948-A 18 02-FEB-2005;
Aguarita Inc. (US)
FEATURES Location/Qualifiers
source 1..18

"/organism="synthetic construct"
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/note="Description of Artificial Sequence: Primer"

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Query Match 91.1%; Score 16.4; DB 6; Length 18;
Best Local Similarity 94.4%; Pred. No. 5.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCCCTCTTGATAC 18
1 CCCCCCTCTTGATAC 18

Db 1 CCCCCCTCTTGATAC 18

RESULT 5
AX316109 18 bp DNA linear PAT 14-DEC-2001
LOCUS AX316109
DEFINITION Sequence 18 from Patent WO0190312.
ACCESSION AX316109
VERSION AX316109.1 GI:17899300
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Hovanec, T.A. and Burrell, P.C.
TITLE Ammonia-oxidizing bacteria
JOURNAL Patent: WO 0190312-A 18 29-NOV-2001;
AQUARIA, INC. (US)
FEATURES Location/Qualifiers
source 1..18
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Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCCCTCTTGATAC 18
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Db 1 CCCCCCTCTTGATAC 18

RESULT 6
AR083535 30 bp DNA linear PAT 01-SEP-2000
LOCUS AR083535
DEFINITION Sequence 74 from patent US 5976873.
ACCESSION AR083535
VERSION AR083535.1 GI:10010308
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Bohinek, R.J. and Whiteett, J.A.
TITLE Nucleic acid sequences controlling lung cell-specific gene
expression
JOURNAL Patent: US 5976873-A 74 02-NOV-1999;
FEATURES Location/Qualifiers
source 1..30
"/organism="unknown"
/mol_type="unassigned DNA"

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Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CCCCCCTCTTGATAC 17

Db 24 CCCCCCTACTGGATA 9

RESULT 7				
CQ796928				
LOCUS	CQ796928	18 bp	DNA	linear
DEFINITION	Sequence 21 from Patent WO2004026772.			PAT 19-APR-2004
ACCESSION	CQ796928			
VERSION	CQ796928.1	GI:46408554		
KEYWORDS				
SOURCE	synthetic construct			

REFERENCE	1
AUTHORS	Hovaneec, T. A.
TITLE	Ammonia-oxidizing bacteria and methods of using and detecting the same
JOURNAL	Patent: WO 2004026772-A 21 01-APR-2004; Aquaria Inc. (US)
FEATURES	location/Qualifiers
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				Indels 0;
				Gaps 0;
QY	2	CCCCCTTCGAGTAC	18	
Db	2	CCCCCAGCTTCGAGCAC	18	

ORIGIN

Query March	76.7%	Score 13.8	DB 6	Length 28
Best Local Similarity	88.2%	Pred. 0.1.5e+04		
Matches 15, Conservative	0	Mismatches 2	Indels 0	Gaps 0

RESULT 9			
AR568743			
LOCUS			
DEFINITION			
AR568743	17 bp	DNA	linear
Sequence 17 from patent US 6740735.			PAT 14-DEC-2004

ACCESSION	AR568743
VERSION	AR568743.1
KEYWORDS	GI:56568296
SOURCE	Unknown.

REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES	SOURCE
1	(bases 1 to 17)	Unclassified.			
	Gianturco, S. H. and Bradley, W. A.	DNA encoding human apoB48: a monocyte-macrophage apolipoprotein			
	B48 receptor gene and protein	Patent: US 6740735-A 17 25-MAY-2004;			
	Location/Qualifiers				
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	/organism="unknown"				
	/mol_type="genomic DNA"				

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BD254227	
LOCUS	BD254227 17 bp DNA linear PAT 17-JUL-2009
DEFINITION	Regulation of repressor genes using nucleic acid molecules.
ACCESSION	BD254227
VERSION	BD254227.1 GI:33063997
KEYWORDS	CP 2002541795-A/2020.
SOURCE	unidentified
ORGANISM	unidentified

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QY	2	CCCCCTCTTCGA	15	
db	3	CCCCCTCTCCTGA	16	

RESULT 11
BD254228 17 bp DNA linear PAT 17-JUL-2003
LOCUS BD254228
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION BD254228.1 GI:33063998
VERSION JP 2002541795-A/2021.
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unidentified

REFERENCE
1 (bases 1 to 17)
Blatt, L., Zwick, M., Pavco, P. and Mcswigen, J.
AUTHORS Regulation of repressor genes using nucleic acid molecules
TITLE Patent: JP 2002541795-A 2021 10-DEC-2002;
JOURNAL RIBOZYME PHARMACEUTICALS INC

COMMENT
OS Eukaryote
PN JP 2002541795-A/2021
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC
C12N15/09, A61K38/00, A61P43/00, A61P43/00, C12N5/10, PC
C12P21/02,
PC C12P21/02, C12P21/02//A61K31/711, (C12N5/10, C12R1:91), (C12P21/02, PC
C12R1:91)
PC (C12P21/02, C12R1:91), (C12P21/02, C12R1:91), C12N15/00, C12N5/00,
PC A61K37/02,
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Key source location/Qualifiers
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location/Qualifiers
1.17
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ORIGIN

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Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCCCCTCTTCGGA 15
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RESULT 12
CQ801520/c 20 bp DNA linear PAT 05-MAY-2004
LOCUS CQ801520
DEFINITION Sequence 30 from Patent WO2004033723.
ACCESSION CQ801520
VERSION CQ801520.1 GI:47058110
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE
1
Mitchell, J. and de Bellecoche, J.
AUTHORS Neurodegenerative disease-associated gene
TITLE Patent: WO 2004033723-A 30 22-APR-2004;
JOURNAL IMPERIAL COLLEGE INNOVATIONS LIMITED (GB)
COMMENT location/Qualifiers
1.20
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

FEATURES
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ORIGIN

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Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCCCCTCTTCGGA 15
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18 CCCCCTCTTCGGA 5
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Db

RESULT 13
AR311956 20 bp DNA linear PAT 12-JUN-2003
LOCUS AR311956
DEFINITION Sequence 2493 from patent US 6559294.
ACCESSION AR311956
VERSION AR311956.1 GI:31705382
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE
1 (bases 1 to 20)
Griffiths, R., Hoiseh, S.K., Zagureky, R.J., Metcalf, B.J., Peek, J.A.,
AUTHORS Sankaran, B. and Fletcher, L.D.
TITLE Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL Patent: US 6559294-A 2493 06-MAY-2003;
Genet, S.A.;;
FRX;

FEATURES
source location/Qualifiers
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/organism="unknown"
/mol_type="genomic DNA"

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Best Local Similarity 92.9%; Pred. No. 9.2e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CCTCTTCGATAC 18
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4 CCTCTTCGATTC 17
|||||

Db

RESULT 14
BD197714 17 bp RNA linear PAT 17-JUL-2003
LOCUS BD197714
DEFINITION Method and reagent for treating diseases or conditions concerning
ACCESSION molecule participating in vasculogenic response.
VERSION BD197714.1 GI:33007484
KEYWORDS JP 2002509721-A/740.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE
1 (bases 1 to 17)
Pavco, P.A., Roberts, B., Jarvie, T., Coeshott, C. and Mcswigen, J.A.
AUTHORS Method and reagent for treating diseases or conditions concerning
TITLE molecule participating in vasculogenic response
JOURNAL Patent: JP 2002509721-A 740 02-APR-2002;
COMMENT RIBOZYME PHARMACEUTICALS INC
OS Homo sapiens (human)
PN JP 2002509721-A/740
PD 02-APR-2002
PF 24-MAR-1999 JP 2000541291
PR 27-MAR-1998 US 60/079678
PI PAMELA A PAVCO, ELISABETH ROBERTS, THALE JARVIS, CLAIRE COESHOTT,
PI JAMES A MCSWIGGEN
PC C12N15/09, A61K31/7088, A61K31/7125, A61K48/00, A61P3/10, A61P17/06, PC
A61P23/00,
PC A61P35/00, A61P43/00, C12N5/10, C12N9/00//A61K35/76, C12N15/00, PC

C12N5/00
CC Method and reagent for treating diseases or conditions CC
CC concerning molecule
CC participating in vasculogenic response
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QY 1 CCCCCCTTCTGGATA 17
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Db

RESULT 15

112779 23 bp DNA linear PAT 26-JUL-1995
LOCUS Sequence 77 from patent US 5427930.
ACCESSION 112779
VERSION 112779.1 GI:910161
KEYWORDS
SOURCE
ORGANISM
ORGANISM Unknown.
SOURCE Unknown.
REFERENCE Unclassified.
1 (bases 1 to 23)
AUTHORS Birkenmeyer,L.G., Carrino,J.J., Dille,B.J., Hu,H.-Y.,
Kratovich,J.D., Laffler,T.G., Marshall,R.L., Rinehardt,L.A. and
Solomon,N.A.
TITLE Amplification of target nucleic acids using gap filling ligase
JOURNAL chain reaction
Patent: US 5427930-A 77 27-JUN-1995;
FEATURES Location/Qualifiers
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/mol_type='unassigned DNA'

ORIGIN

Query Match 67.8%; Score 12.2; DB 6; Length 23;
Best Local Similarity 82.4%; Pred. No. 1.2e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CCCCCCTTCTGGATA 18
1 CCCCCCTTCTGGATA 18
Db

Search completed: April 7, 2006, 14:36:14
Job time : 940.432 secs

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 7, 2006, 08:39:12 ; Search time 213.568 Seconds
(without alignments)
561.717 Million cell updates/sec

Title: US-10-659-980A-5

Perfect score: 18
Sequence: 1 cccccctctctgataac 18

Scoring table: OLIGO_NUC
Gapop 60.0, Gapext 60.0

Searched: 4996997 seqs, 332246308 residues

Word size: 11

Total number of hits satisfying chosen parameters: 4138354

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Maximum DB seq length: 30

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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7	12	66.7	17	12	ADDO00840
8	12	66.7	18	6	ABA02421
9	12	66.7	18	12	ADM322709
10	12	66.7	19	4	AAF86277
11	12	66.7	19	10	ADB10102
12	12	66.7	20	2	AAK14630
13	12	66.7	20	2	AAK93192
14	12	66.7	20	6	AAK93192
15	12	66.7	20	10	ABK13323
16	12	66.7	20	11	ADM65292
17	12	66.7	20	11	ADP75325
18	12	66.7	20	12	ADM16243
19	12	66.7	20	12	ADQ10092

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C	23	12	66.7	25	9	ACH57541	ACH57541 DNA target
C	24	12	66.7	25	10	ADE10105	Adel0105 Mutagenic
C	25	12	66.7	30	14	ADY03371	Ady03371 PCR prime
C	26	11	61.1	13	5	ABF89343	ABF89343 Oligonuc
C	27	11	61.1	13	5	ABF89342	ABF89342 Oligonuc
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C	34	11	61.1	18	4	AAH78146	AAH78146 PCR prime
C	35	11	61.1	18	4	AAF79606	AAF79606 Human Akt
C	36	11	61.1	18	6	ABA04522	ABA04522 PCR prime
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C	40	11	61.1	19	6	AAK98029	AAK98029 Murine SA
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ALIGNMENTS

RESULT 1	ABA02420	standard; DNA; 18 BP.
ID	ABA02420	
XX	ABA02420;	
AC	29-AUG-2003 (revised)	
XX	04-MAR-2002 (first entry)	
DT	29-AUG-2003 (revised)	
DT	04-MAR-2002 (first entry)	
XX	Type A/A1 ammonia-oxidising bacterium 16S rRNA gene probe.	
DB	Type A; type A1, ammonia-oxidising bacterium; AOB; nitrite;	
KW	16S rRNA gene; ribosomal RNA; aquarium; aquaculture;	
KW	waste water treatment; bioremediation; probe; ss.	
XX	Nitrosomonadales.	
OS		
XX		
PN	NO200190312-A1.	
XX		
PD	29-NOV-2001.	
XX		
PF	17-MAY-2001; 2001MO-US016265.	
XX		
PR	19-MAY-2000; 2000US-00573684.	
XX		
PA	(AQUA-) AQUARIA INC.	
PI	Hovanec TA, Burrell PC;	
XX	WPI; 2002-075367/10.	
DR		
XX		
PT	New bacteria capable of oxidizing ammonia to nitrite, for preventing or	
PT	alleviating the accumulation of ammonia in fresh water aquaria, seawater	
PT	aquaria and waste water.	
XX		
PS	Claim 26; Page 53; 62pp; English.	
XX		
CC	The invention relates to 4 novel types of ammonia-oxidising bacteria	
CC	(AOB) found in freshwater aquaria. The bacteria are able to oxidise	
CC	ammonia to nitrite and are members of the ammonia-oxidising bacteria	
CC	family of the beta subdivision of Proteobacteria. The 4 types of bacteria	
CC	can be distinguished on the basis of their 16S rRNA (ribosomal RNA) gene	

CC sequences (ABA02416-ABA02419), and are classified as AOB type A (e.g.,
CC R7clone140), type A1 (e.g., R7clone187), type B (e.g., R3clones) and type
CC C (e.g., R3clone417). The invention also encompasses isolated 16S rRNA
CC gene sequences of the ammonia-oxidising bacteria of the invention,
CC oligonucleotide probes and primers for the detection of these bacteria,
CC and compositions comprising the bacteria. The bacteria of the invention
CC are useful in biological filters for reducing ammonia accumulation in
CC both freshwater and seawater aquaria. They may also be used in waste
CC water treatment and in bioremediation processes to reduce the level of
CC pollution caused by ammonia. The present sequence represents a
CC specifically claimed probe for the detection of the 16S rRNA gene
CC sequences of the type A and A1 ammonia-oxidising bacteria (ABA02416-
CC ABA02417). (updated on 29-AUG-2003 to standardise OS field)
XX
SQ Sequence 18 BP, 2 A, 9 C, 2 G, 5 T, 0 U, 0 Other;

Query Match 100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCCCTCTTCGGATAC 18
1 CCCCCCTCTTCGGATAC 18
DB 1 CCCCCCTCTTCGGATAC 18

RESULT 2
ADM32708
ID ADM32708 standard; DNA; 18 BP.
XX
AC ADM32708;
XX
DT 17-JUN-2004 (first entry)
XX
DE Nitrosospira-like 16S rDNA probe. S-G-Nsapa-0149-a-a-18.
XX
KM 16S rDNA; ammonia oxidising bacteria; AOB; ammonia; nitrite;
XX aqueous environment; freshwater; seawater; aquarium; ser. probe.
XX
OS Nitrosospira sp.
XX
PN MO2004026772-A2.
XX
PD 01-APR-2004.
XX
PF 10-SEP-2003; 2003MO-US028210.
XX
PR 19-SEP-2002; 2002US-0386217P.
XX 19-SEP-2002; 2002US-0386218P.
XX 19-SEP-2002; 2002US-0386219P.
XX
PA (AOBA-) AQUARIA INC.
XX
PI Hovanec TA;
XX
PT MPI; 2004-304936/28.
XX
PS
XX
PT New composition comprising an isolated bacterial strain that oxidizes
XX ammonia to nitrite, useful for alleviating or preventing the accumulation
XX of ammonia in aqueous environment.
XX
PS Example 6; Page 34; 99pp; English.
XX
CC This sequence represents a probe which was used in the detection of 16S
CC rDNA sequence derived from an ammonia oxidising bacteria (AOB). The
CC amplified sequence may be used in a composition which comprises an
CC isolated bacterial strain that oxidizes ammonia to nitrite. The
CC composition may be used for alleviating or preventing the accumulation of
CC ammonia in a medium. The ammonia is reduced by at least 30% when compared
CC with a level of ammonia that would exist in the absence of the bacterial
CC strain. The composition is useful for alleviating or preventing the
CC accumulation of ammonia in aqueous environment, e.g. a freshwater or
CC seawater aquarium.
XX

SQ Sequence 18 BP; 2 A; 9 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCCCTCTTCGGATAC 18
1 CCCCCCTCTTCGGATAC 18
DB 1 CCCCCCTCTTCGGATAC 18

RESULT 3
ABT39927
ID ABT39927 standard; DNA; 17 BP.
XX
AC ABT39927;
XX
DT 13-JUN-2003 (first entry)
XX
DE Tumour suppression related human fukutin oligo SEQ ID No 5564.
XX
XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
XX antitense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
XX schizoprenia; protein chip; gene therapy; tumour suppression;
XX human fukutin; ds.
XX
XX Homo sapiens.
XX
OS
XX
PN MO2003025175-A2.
XX
PD 27-MAR-2003.
XX
PF 17-SEP-2002; 2002MO-IB004208.
XX
PR 17-SEP-2001; 2001PR-00011978.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX
DR MPI; 2003-31353/30.
XX
PT New isolated nucleic acid, useful for treating viral diseases associated
XX with tumors and cell degeneration, also related polypeptides, antibodies
XX and transfected cells.
XX
PS Disclosure; Page 684; 720pp; French.
XX
XX The invention relates to a novel isolated 17 mer nucleic acid sequence,
XX given in the specification, a sequence containing at least 15 consecutive
XX nucleotides from the 17 mer sequence, a sequence with, after optimal
XX alignment, at least 80 % identity to the 17 mer sequence, a sequence that
XX hybridizes to them under highly stringent conditions, or the complement
XX of any of them, or the corresponding RNA. The novel isolated nucleic
XX acids of the invention are useful as probes and primers for detecting,
XX identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
XX component of a gene chip, in vitro as (anti)sense reagents, and for
XX production of recombinant polypeptides. Any of the nucleic acids,
XX polypeptides, vectors containing the nucleic acids, cells containing the
XX vector or antibodies directed against the polypeptides are useful for
XX preparation of pharmaceuticals for prevention and/or treatment of viral
XX diseases that are characterised by development of tumours or cell
XX degeneration, specifically cancer but also Alzheimer's disease and
XX schizoprenia. Analaysis of the expression and/or prognosis of these
XX diseases. The polypeptides can also be used to generate antibodies, and
XX both the polypeptide and antibodies are useful as components of protein
XX chips. The nucleic acid sequences of the invention can be used in gene
XX therapy. This polynucleotide sequence represents a tumour suppression
XX related human fukutin oligonucleotide of the invention
SQ Sequence 17 BP; 5 A; 4 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 66.7%; Score 12; DB 8; Length 17;
 Best Local Similarity 100.0%; Pred. No. 7.5e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 TCTTCTGGATAC 18
 |||||
 DB 3 TCTTCTGGATAC 14

RESULT 4

ACC67980
 ID ACC67980 standard; DNA; 17 BP.

AC 667980;
 AC 667980;

DT 01-JUN-2003 (first entry)

DE Murine oligonucleotide associated with tumour suppression, SEQ ID 5227.

XX Cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; murine;
 KM tumour suppression; tumour reversion; apoptosis; virus resistance;
 KM viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
 KM schizophrenia; ss.

XX schizophrentia; ss.
 OS Mus musculus.

OS Mus musculus.

PN WO2003025176-A2.

XX 27-MAR-2003.

XX 17-SEP-2002; 2002WO-IB004210.

XX 17-SEP-2001; 2001FR-00011979.

XX (MOLR-) MOLECULAR ENGINES LAB.

XX Telerman A, Amson R, Tuijnder M;

XX WPI; 2003-333167/31.

XX New isolated nucleic acid, useful for treating viral diseases associated
 PT with tumors and cell degeneration, also related polypeptides, antibodies
 PT and transfected cells.

XX Disclosure; Page 642; 738pp; French.

XX The present invention relates to murine oligonucleotides (ACC62754-
 CC ACC68906), which are associated with tumour suppression, tumour

CC reversion, apoptosis and virus resistance. The oligonucleotides are
 CC useful as (1) as probes and primers for detecting, identifying,

CC quantifying and/or amplifying nucleic acid, e.g. as one component of a
 CC gene chip; in vitro as (anti)sense reagents; and (2) for production of

CC recombinant polypeptides. The oligonucleotides are useful for preparation
 CC of pharmaceuticals for prevention and/or treatment of viral diseases that

CC are characterized by development of tumour or cell degeneration,
 CC specifically cancer but also Alzheimer's disease and schizophrenia

XX Sequence 17 BP; 1 A; 6 C; 4 G; 6 T; 0 U; 0 Other;

XX Query Match 66.7%; Score 12; DB 8; Length 17;
 Best Local Similarity 100.0%; Pred. No. 7.5e+03;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCCTCTTCTGG 14
 |||||
 DB 4 CCCCTCTTCTGG 15

DB 4 CCCCTCTTCTGG 15

RESULT 5

ADH43132
 ID ADH43132 standard; DNA; 17 BP.

AC ADH43132;

XX ADH43132;

XX 18-DEC-2003 (revised)
 DT 04-DEC-2003 (first entry)

XX Tumour suppression/reversion associated nucleotide #3455.

XX Cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
 KM primer; probe; tumour suppression; tumour reversion; apoptosis;
 KM virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
 KM diagnosis.

XX Homo sapiens.

OS Homo sapiens.

PN WO2003040369-A2.

XX 15-MAY-2003.

XX 17-SEP-2002; 2002WO-IB004219.

XX 17-SEP-2001; 2001FR-00011981.

XX (MOLR-) MOLECULAR ENGINES LAB.

XX Telerman A, Amson R, Tuijnder M;

XX WPI; 2003-441574/41.

XX New nucleic acid encoding human prostate membrane-specific antigen,
 PT useful e.g. for treatment of tumors and viral infection, also related
 PT polypeptide and antibodies.

XX Disclosure; Page 435; 771pp; French.

XX The invention relates to the isolation of 6327 nucleotide sequences,
 CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
 CC sequence having at least 80% identity, after optimal alignment, with the
 CC nucleotides, a sequence that hybridizes under stringent conditions with

CC the nucleotides, or the complement, or corresponding RNA, of the
 CC nucleotides. The nucleotides are used as probes or primers for detecting,
 CC identifying, quantifying and/or amplifying nucleic acids, as in vitro

CC sense and antisense sequences, of nucleotides involved in tumour
 CC suppression or reversion, apoptosis and or viral resistance, to produce

CC recombinant polypeptides, and to prepare transgenic animals, as
 CC experimental models. The nucleotides (also vectors containing them and

CC cells containing the vectors), the encoded polypeptides and antibodies
 CC (Ab) against the polypeptide are useful for prevention and/or treatment

CC of viral infections or diseases characterized by development of tumours
 CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).

CC Analysis of the expression of the nucleotides can be used for diagnosis
 CC and/or prognosis of these diseases. The nucleotides and polypeptides can

CC also be used to screen for their specific interactive molecules,
 CC potentially useful for treating diseases associated with abnormal

XX expression of the nucleotides.

XX Sequence 17 BP; 5 A; 4 C; 3 G; 5 T; 0 U; 0 Other;

XX Query Match 66.7%; Score 12; DB 10; Length 17;
 Best Local Similarity 100.0%; Pred. No. 7.5e+03;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 TCTTCTGGATAC 18
 |||||
 DB 3 TCTTCTGGATAC 14

DB 3 TCTTCTGGATAC 14

DB 3 TCTTCTGGATAC 14

DB 3 TCTTCTGGATAC 14

ADH30251
 ID ADH30251 standard; DNA; 17 BP.

AC ADH30251;

XX 11-MAR-2004 (first entry)

DE Human monocyte-macrophage cell surface apob48 receptor primer #5.
 XX anti11pemic; gene therapy;
 KW monocyte-macrophage cell surface apob48 receptor; apob48R;
 KM pattern B phenotype; familial combined hyperlipidaemia;
 KW hypercholesterolaemia; hypertriglyceridaemia;
 KM low plasma high-density lipoprotein level; human; primer; ss.
 XX Homo sapiens.
 XX US2003208060-A1.
 XX 06-NOV-2003.
 XX 12-JUN-2003; 2003US-00459876.
 XX 06-AUG-1998; 98US-00130242.
 PR 31-MAY-2000; 2000US-00583610.
 XX (GIAN/) GIANTURCO S H.
 PA (BRAD/) BRADLEY W A.
 PI Gianturco SH, Bradley WA;
 DR WPI; 2003-864799/80.
 XX New isolated DNA molecule encoding a monocyte-macrophage cell surface
 PT apob48 receptor protein (apob48R), useful in preparing a composition for
 PT treating e.g., familial or non-familial hypercholesterolemia.
 XX Example 23; SEQ ID NO 17; 77pp; English.
 CC The invention describes a new isolated DNA molecule, encoding a monocyte-
 CC macrophage cell surface apob48 receptor protein (apob48R) comprising a
 CC fully defined 1088 amino acid sequence. The DNA molecule is useful in
 CC preparing a composition for treating Pattern B phenotype, familial
 CC combined hyperlipidaemia, familial or non-familial hypercholesterolemia,
 CC hypertriglyceridaemia or low plasma high-density lipoprotein levels. This
 CC sequence represents a primer used in the isolation of human monocyte-
 CC macrophage cell surface apob48 receptor DNA.
 XX Sequence 17 BP; 2 A; 6 C; 4 G; 5 T; 0 U; 0 Other;
 SO
 Query Match 66.7%; Score 12; DB 10; Length 17;
 Best Local Similarity 100.0%; Pred. No. 7.5e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 CCTCTCTGGAT 16
 DB 5 CCTCTCTGGAT 16
 RESULT 7
 ADO00840
 ID ADO00840 standard; DNA; 17 BP.
 AC ADO00840; Y
 XX 12-AUG-2004 (first entry)
 DE Human monocyte-macrophage cell surface apob48R cDNA PCR primer #6.
 XX Human; monocyte-macrophage cell surface apolipoprotein B 48 receptor;
 KW apolipoprotein B 48 receptor; apob48R; PCR; ss; monocyte; macrophage;
 KW reticuloendothelial cell; monocyte adhesion; cardiovascular disease;
 KW apob-mediated cellular uptake; plasma chylomicron;
 KW hypertriglyceridaemia; triglyceride-rich lipoprotein;
 KM apob independent pathway; lipoprotein lipase independent pathway;
 KW heparin sulfate proteoglycan independent pathway; foam cell formation;
 KW hypertriglyceridaemia; primer.
 XX Homo sapiens.
 XX

PN US6740735-B1.
 XX 25-MAY-2004.
 PD 31-MAY-2000; 2000US-00583610.
 PF 06-AUG-1998; 98US-00130242.
 XX (GIAN/) GIANTURCO S H.
 PA (BRAD/) BRADLEY W A.
 PI Gianturco SH, Bradley WA;
 DR WPI; 2004-387250/36.
 XX New isolated monocyte-macrophage cell surface apob48 receptor protein,
 PT useful for cell-specific delivery of therapeutic compounds to human
 PT monocytes or macrophages, or for evaluating an individual at risk for
 PT cardiovascular disease.
 XX Example 23; SEQ ID NO 17; 72pp; English.
 CC The invention relates to the human monocyte-macrophage cell surface
 CC apolipoprotein B 48 receptor (apob48R) protein and the nucleic acid
 CC encoding it. The invention also relates to a method of cell-specific
 CC delivery of therapeutic compounds to human monocytes, macrophages or
 CC other reticuloendothelial cells that express the receptor, a method of
 CC inhibiting foam cell formation and increased monocyte adhesion to
 CC endothelial cells and a method of evaluating an individual at risk of a
 CC cardiovascular disease. The monocyte-macrophage cell surface apob48
 CC receptor protein is useful in the apob-mediated cellular uptake of plasma
 CC chylomicrons and remnants and hypertriglyceridaemic triglyceride-rich
 CC lipoproteins in an apob independent pathway, a lipoprotein lipase
 CC independent pathway or a heparin sulfate proteoglycan independent
 CC pathway. It is also useful for the cell-specific delivery of therapeutic
 CC compounds to human monocytes, macrophages or other reticuloendothelial
 CC cells that express the receptor, for inhibiting foam cell formation and
 CC increased monocyte adhesion to endothelial cells and for evaluating an
 CC individual at risk of a cardiovascular disease such as
 CC hypertriglyceridaemia. This sequence represents a PCR primer used in
 CC cloning of cDNA encoding the apob48R protein of the invention.
 XX Sequence 17 BP; 2 A; 6 C; 4 G; 5 T; 0 U; 0 Other;
 SO
 Query Match 66.7%; Score 12; DB 12; Length 17;
 Best Local Similarity 100.0%; Pred. No. 7.5e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 CCTCTCTGGAT 16
 DB 5 CCTCTCTGGAT 16
 RESULT 8
 ABA02421/C
 ID ABA02421 standard; DNA; 18 BP.
 AC ABA02421;
 XX 29-AUG-2003 (revised)
 DT 04-MAR-2002 (first entry)
 DE Type A/1 ammonia-oxidising bacterium 16S rRNA gene forward PCR primer.
 XX Type A; type A1; ammonia-oxidising bacterium; AOB; nitrite;
 KW 16S rRNA gene; ribosomal RNA; aquarium; aquaculture;
 KW waste water treatment; bioremediation; PCR primer; ss.
 XX Nitrosomonadales.
 OS
 XX WO200190312-A1.
 PN 29-NOV-2001.
 PD

XX 17-MAY-2001; 2001WO-US016265.
 PF 19-MAY-2000; 2000US-00573684.
 XX (AQUA-) AQUARIA INC.
 PA Hovanec TA, Burrell PC;
 PI WPI; 2002-075367/10.
 DR
 XX New bacteria capable of oxidizing ammonia to nitrite, for preventing or
 PT alleviating the accumulation of ammonia in fresh water aquaria, seawater
 PT aquaria and waste water.
 XX
 PS Example; Page 10; 62pp; English.
 XX
 CC The invention relates to 4 novel types of ammonia-oxidizing bacteria
 CC (AOB) found in freshwater aquaria. The bacteria are able to oxidize
 CC ammonia to nitrite and are members of the ammonia-oxidizing bacteria
 CC family of the beta subdivision of Proteobacteria. The 4 types of bacteria
 CC can be distinguished on the basis of their 16S rRNA (ribosomal RNA) gene
 CC sequences (ABA02416-ABA02419), and are classified as AOB type A (e.g.,
 CC R7clone140), type A1 (e.g., R7clone187), type B (e.g., R3clone5) and type
 CC C (e.g., R3clone47). The invention also encompasses isolated 16S rRNA
 CC gene sequences of the ammonia-oxidizing bacteria of the invention.
 CC oligonucleotide probes and primers for the detection of these bacteria,
 CC and compositions comprising the bacteria. The bacteria of the invention
 CC are useful in biological filters for reducing ammonia accumulation in
 CC both freshwater and seawater aquaria. They may also be used in waste
 CC water treatment and in bioremediation processes to reduce the level of
 CC pollution caused by ammonia. Sequences ABA02421-ABA02422 represent PCR
 CC primers for the detection of the 16S rRNA gene sequences of the type A
 CC and A1 ammonia-oxidizing bacteria (ABA02416-ABA02417). (Updated on 29-AUG
 CC -2003 to standardise OS field)
 CC
 SQ Sequence 18 BP; 7 A; 4 C; 5 G; 2 T; 0 U; 0 Other;
 XX
 QY Query Match 66.7%; Score 12; DB 6; Length 18;
 Best Local Similarity 100.0%; Pred. No. 7.5e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 7 TCTTCGTGATAC 18
 18 TCTTCGTGATAC 7
 XX
 RESULT 9
 ADM32709/c
 ID ADM32709 standard; DNA; 18 BP.
 AC ADM32709; Y.
 AC
 DT 17-JUN-2004 (first entry)
 XX
 DE Type A AOB 16S rDNA forward primer.
 XX
 KW 16S rDNA; ammonia oxidizing bacteria; AOB; ammonia; nitrite;
 KW aqueous environment; freshwater; seawater; aquarium; ss; primer.
 XX
 OS Nitrosomonas aestuarii.
 XX
 PN WO2004026772-A2.
 XX
 PD 01-APR-2004.
 XX
 PF 10-SRP-2003; 2003WO-US026210.
 XX
 PR 19-SRP-2002; 2002US-0386217P.
 PR 19-SRP-2002; 2002US-0386218P.
 PR 19-SRP-2002; 2002US-0386219P.
 XX
 PA (AQUA-) AQUARIA INC.

XX Hovanec TA;
 XX WPI; 2004-304936/28.
 DR
 XX New composition comprising an isolated bacterial strain that oxidizes
 PT ammonia to nitrite, useful for alleviating or preventing the accumulation
 PT of ammonia in aqueous environment.
 XX
 PS Example 7; Page 34; 98pp; English.
 XX
 CC This sequence represents a primer which was used in the detection of 16S
 CC rRNA sequence derived from an ammonia oxidizing bacteria (AOB). The
 CC amplified sequence may be used in a composition which comprises an
 CC isolated bacterial strain that oxidizes ammonia to nitrite. The
 CC composition may be used for alleviating or preventing the accumulation of
 CC ammonia in a medium. The ammonia is reduced by at least 30% when compared
 CC with a level of ammonia that would exist in the absence of the bacterial
 CC strain. The composition is useful for alleviating or preventing the
 CC accumulation of ammonia in aqueous environment, e.g. a freshwater or
 CC seawater aquarium.
 CC
 SQ Sequence 18 BP; 7 A; 4 C; 5 G; 2 T; 0 U; 0 Other;
 XX
 QY Query Match 66.7%; Score 12; DB 12; Length 18;
 Best Local Similarity 100.0%; Pred. No. 7.5e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 7 TCTTCGTGATAC 18
 18 TCTTCGTGATAC 7
 XX
 RESULT 10
 AAF6277/c
 ID AAF6277 standard; DNA; 19 BP.
 AC AAF6277;
 AC
 DT 24-JUL-2001 (first entry)
 XX
 DE Mutated cPPT fragment cPPT-225 SEQ ID 23.
 XX
 KW Triplex; cis-polypurine tract; cPPT; central termination sequence; CTS;
 KW cis acting region; retrovirus; blood disorder; developmental disorder;
 KW brain disorder; nervous system disorder; ss.
 XX
 OS Human immunodeficiency virus 1.
 OS Synthetic.
 OS
 PN WO200127304-A2.
 PN
 PD 19-APR-2001.
 PD
 PF 10-OCT-2000; 2000WO-BP010418.
 XX
 PR 12-OCT-1999; 99US-0158387P.
 XX
 PA (INSP) INST PASTEUR.
 PA (INRM) INST NAT SANTE & RECH MEDICALE.
 XX
 PI Charneau P, Zennou V, Pflumio F, Silven A, Dubart Kupperschmitt A;
 XX WPI; 2001-273782/28.
 DR
 XX New nucleic acid, useful for prophylactic, ameliorative or curative
 PT treatment of genetic diseases, comprises retroviral cis-polypurine tract
 PT and central termination sequence cis acting regions.
 XX
 PS Example 2; Fig 1A; 81pp; English.
 XX
 CC This invention relates to a triple stranded nucleic acid structure
 CC containing at least one copy of the cis-polypurine tract (cPPT) and

CC central termination sequence (CTS) cis acting regions of a retrovirus.
CC The cPPT region initiates synthesis of a downstream plus strand during
CC reverse transcription and CTS is involved in the termination and ejection
CC of reverse transcriptase. The cPPT and CTS regions induce a 3-stranded
CC DNA structure which stimulates entry of nucleic acids into the nucleus of
CC cells. The triple structures can act as nucleic acid importers into non-
CC dividing target cells. The nucleic acid, and vectors containing it are
CC useful for the prophylactic, ameliorative or curative treatment of an
CC individual suffering from or having a high likelihood of developing a
CC disease or disorder with a genetic basis. Therapeutic proteins can be
CC administered to a patient using a vector containing DNA encoding the
CC protein and the nucleotide sequence of the invention. Diseases and
CC disorders which can be treated include blood disorders, brain or nervous
CC system disorders or developmental disorders. The present sequence
CC represents a mutated fragment of the HIV-1 cPPT sequence. Wild type cPPT
CC and various mutant versions of cPPT are used in an example illustrating
CC that central initiation of reverse transcription is an essential step of
CC the HIV-1 replicative cycle

XX SQ Sequence 19 BP, 7 A, 0 C, 8 G, 4 T, 0 U, 0 Other;

Query Match 66.7%; Score 12; DB 4; Length 19;

Best Local Similarity 100.0%; Pred. No. 7.5e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCCCTCTTCT 12

DB 19 CCCCCCTCTTCT 8

RESULT 11
ADE10102/c
ID ADE10102 standard; DNA; 19 BP.

XX ADE10102;

DT 29-JAN-2004 (first entry)

DE DNA encoding HIV-1 cPPT mutant (cPPT-AG) peptide.

XX LentiVirus; HIV-1; polypurine tract cis-active; cPPT;

KM central termination sequence; CTS; three-stranded DNA;

KM triplex DNA structure.; gene therapy; brain disease;

XX developmental disease; neuroprotective; gene therapy; mutant; ds.

OS Synthetic.
OS Human immunodeficiency virus 1.

XX Key

FT CDS

FT 1..19 Location/Qualifiers
FT /*tag= a
FT /partial
FT /note= "This sequence lacks both start and stop codons"
FT /transl_except= (pos:1..aa:asn)
FT /note= "This codon has an apparent 2 nucleotide deletion
FT which alters the reading frame"

XX US2003194392-A1.

XX 16-OCT-2003.

XX 10-APR-2002; 2002US-00122114.

XX 10-APR-2002; 2002US-00122114.

XX (CHAR/) CHARNEAU P.

XX (ZENN/) ZENNOU V.

XX (PFLU/) PFLUMIO F.

XX (SIRV/) SIRVEN A.

XX (KUPP/) DUBART KUPPERSCHMITT A.

XX Charneau P, Zenou V, Pflumio F, Sirven A, Dubart Kupperschmitt A;

DR WPI; 2003-844442/78.
DR P-PSDB; ADE10101.

XX New nucleic acid comprising at least one copy of the cPPT and CTS cis-
XX acting regions of a retrovirus that induce a three-stranded DNA
XX structure, useful for preparing a composition for treating e.g., brain or
XX developmental disease.

XX Example 2; Fig 1A; 42bp; English.

XX The present invention relates to the isolation of a lentiviral
XX polynucleotide (e.g. HIV-1) polypurine tract cis-active (cPPT) and
XX central termination sequence (CTS) cis-acting regions that induce a three
XX stranded or triplex DNA structure. The lentiviral polynucleotide
XX sequences are useful in gene therapy for preparing a composition for
XX treating an individual suffering from, or having a likelihood of
XX developing a disorder such as brain or developmental disease. The present
XX sequence encodes a mutant HIV-1 cPPT peptide.

XX SQ Sequence 19 BP, 7 A, 0 C, 8 G, 4 T, 0 U, 0 Other;

Query Match 66.7%; Score 12; DB 10; Length 19;

Best Local Similarity 100.0%; Pred. No. 7.5e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCCCTCTTCT 12

DB 19 CCCCCCTCTTCT 8

RESULT 12
AAK14630/c
ID AAK14630 standard; DNA; 20 BP.

XX AAK14630;

DT 24-MAR-1999 (first entry)

DE Triplex helix forming nucleotides 2407-2426 of the n-myc gene.

XX Triplex-helix forming region; Triplex formation; DNA detection;

KM identification; bacteria; oncogene; virus; ds.

XX Homo sapiens.

OS US5861244-A.

XX 19-JAN-1999.

XX 22-DEC-1993; 93US-00173489.

XX 29-OCT-1992; 92US-00968436.

XX (PROF-) PROFILE DIAGNOSTIC SCI INC.

XX Hepburn AG, Wang C;

XX WPI; 1999-130384/11.

XX Assay of genetic sequences based on triplex formation from double
XX stranded analyte - and hybrid of anchor and reporter sequences, with
XX reporter released if triplex formation occurs, used e.g. to identify
XX bacteria.

XX Disclosure; Col 13-14; 168pp; English.

XX The present sequence represents a potential triplex-helix forming region.
XX It can be used to demonstrate the assay of the invention. The assay
XX comprises adding a sample containing double-stranded DNA test sequences,
XX e.g. containing the present sequence, to an aqueous medium containing at
XX least one complex of anchor DNA, attached to a solid support, and
XX reporter DNA, where either a part of the anchor DNA or reporter DNA is
XX designed to form a triplex-strand structure with part of the test

CC sequence. Triplex formation results in displacement of the reporter DNA
 CC which is detected as an indication of the presence of the DNA test
 CC sequence. The method is used to detect DNA sequences, particularly for
 CC identification of bacteria (by detecting genes for ribosomal RNA) in
 CC clinical samples, but also detection of oncogenes and Hepatitis B virus
 SQ Sequence 20 BP; 7 A; 0 C; 13 G; 0 T; 0 U; 0 Other;

Query Match 66.7%; Score 12; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 7.5e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCCCTCTCT 12
 |||||
 DB 18 CCCCCCTCTCT 7

RESULT 13
 AAX93192
 ID AAX93192 standard; DNA; 20 BP.

AC AAX93192;

DT 13-SEP-1999 (first entry)

DE PCR primer used to amplify an ORF of Chlamydia pneumoniae.

KW Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
 KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
 KW neutralising epitope; PCR primer; ss.

OS Synthetic.

OS Chlamydia pneumoniae.

PN MO927105-A2.

PD 03-JUN-1999.

PF 20-NOV-1998; 98MO-IB001890.

PR 21-NOV-1997; 97PR-00014673.

PR 04-NOV-1998; 98US-0107078P.

PA (GEST) GENSEP1.

PI Griffrais R;

DR WPI; 1999-357842/30.

PT Genome sequence of Chlamydia pneumoniae.

PS Page 1570; Disclosure; 1912pp; English.

CC AAX91991-X97517 represent PCR primers used to amplify open reading frames
 CC and other nucleic acid sequences from the genome of Chlamydia pneumoniae
 CC (see AAX91990). C. pneumoniae causes respiratory disease such as
 CC pneumonia and bronchitis and is thought to be a contributing factor in
 CC heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema
 CC nodosum or pharyngitis. The polypeptides encoded by the open reading
 CC frames of the C. pneumoniae genome (see AAY34584-AAY35879) can be used
 CC in immunogenic compositions as vaccines. Vectors containing C. pneumoniae
 CC nucleotide sequences can also be used as immunogenic compositions,
 CC especially where the vector directs the expression of a neutralising
 CC epitope of C. pneumoniae

SQ Sequence 20 BP; 2 A; 5 C; 5 G; 8 T; 0 U; 0 Other;

Query Match 66.7%; Score 12; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 7.5e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCTCTTCTGGAT 16
 |||||

DB 4 CCTCTTCTGGAT 15

RESULT 14
 ID AAS97903/c
 ID AAS97903 standard; DNA; 20 BP.

AC AAS97903;

DT 12-MAR-2002 (first entry)

DE Murine SACL gene-specific oligonucleotide PCR primer #456.

KW Human; mouse; SACL; carbohydrate; sweetener; ethanol; alcoholism; ss;
 KW obesity; diabetes; transgenic embryo; body tissue; body fluid; pancreas;
 KW blood; tongue; PCR primer; anorectic; antidiabetic; gene therapy;
 KW protein replacement therapy.

OS Mus sp.

PN WO200183749-A2.

PD 08-NOV-2001.

PF 25-APR-2001; 2001WO-US013387.

PR 28-APR-2000; 2000US-0200794P.

PR 28-JUL-2000; 2000US-0221419P.

PR 10-NOV-2000; 2000US-0247443P.

PA (WARN) WARNER LAMBERT CO.

PI (MONN-) MONNELL CHEM SENSES CENT.

PI Bachmanov AA, Beauchamp GK, Chatterjee A, De Jong PJ, Li S, Li X;
 Omen JD, Reed DR, Rose D, Tordoff MG;

DR WPI; 2002-075162/10.

PT Novel isolated polypeptide comprising variant form of mouse or human SACL
 PT polypeptide, and is associated with altered preference for carbohydrates
 PT or other sweeteners, useful for preventing obesity, diabetes, alcoholism.

PS Claim 14; Page 92; 23pp; English.

CC The invention relates to an isolated polypeptide, comprising a variant
 CC form of mouse or human SACL polypeptide. The variant form is associated
 CC with altered preference for carbohydrates, other sweeteners or ethanol.
 CC The polypeptide and its associated DNA sequence can be produced by
 CC recombinant techniques and is useful for preventing obesity, diabetes or
 CC alcoholism associated with SACL expression. The sequences are useful in
 CC screening for drugs and sweeteners. Recombinant cell lines and transgenic
 CC embryos may be used in screening for and identifying agents that induce
 CC or repress function of SACL. Predilection to diabetes, obesity or
 CC alcoholism can be ascertained by testing any fluid or tissue of a human
 CC (such as blood, pancreas or tongue) for sequence variations of the SACL
 CC gene. A sequence variation of the SACL locus may indicate a
 CC predisposition to diabetes, obesity and/or alcoholism and may provide a
 CC diagnostic mark. The polynucleotide can be detected in a biological
 CC sample by contacting the DNA with a probe to form a hybridisation complex
 CC which is then detected. The sequences represent cDNA encoding human and
 CC mouse SACL polypeptides and PCR primers specific for the SACL genes

SQ Sequence 20 BP; 7 A; 6 C; 6 G; 1 T; 0 U; 0 Other;

Query Match 66.7%; Score 12; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 7.5e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCTCTTCTGGA 15
 |||||
 DB 19 CCTCTTCTGGA 8

```

RESULT 15
ID ABX13323/c
XX ABX13323 standard; DNA; 20 BP.
AC
XX ABX13323;
XX
DT 14-MAY-2003 (first entry)
XX
DE Human NSDHL gene, exon 8 PCR primer #4.
XX
XX Human; sex; PCR; 3beta-hydroxysteroid dehydrogenase; 3beta-HSD; NSDHL;
XX cholesterol biosynthesis; mevalonic aciduria; desmosterolosis;
XX Smith-Lemli-Opitz syndrome; SLOS; Conradi-Hunermann-Happle syndrome;
XX chondroplasia punctata; X-linked disease; chromosome Xq28; psoriasis;
XX CHILD syndrome; bone disorder; osteoporosis; osteosclerosis;
XX congenital hemidysplasia; ichthyosiform erythroderma and limb defect;
XX ichthyosis; eye disorder; cataract; microphthalmia; arthritis;
XX cholest-8(9)-en-3beta-ol; skin disorder; primer.
XX
OS Homo sapiens.
XX
XX US2002172956-A1.
XX
XX 21-NOV-2002.
XX
XX 05-SEP-2001; 2001US-00946406.
XX
XX 01-JUN-1999; 99US-0137020P.
XX
XX 01-JUN-2000; 2000US-00588976.
XX
XX
XX (CHILD-) CHILDRENS HOSPITAL INC.
XX
XX Herman GE, Kelley RI, Grange DK;
XX
XX WPI; 2003-310984/30.
XX
XX
XX Diagnosing CHILD syndrome or psoriasis, by detecting differences between
XX patient and wild type genes encoding 3 beta-hydroxysteroid dehydrogenase
XX or accumulation of sterol intermediates in body fluids of the patient.
XX
XX
XX Disclosure; Page 2; 23pp; English.
XX
XX
XX The invention relates to diagnosing congenital hemidysplasia,
XX ichthyosiform erythroderma and limb defects (CHILD) syndrome or psoriasis
XX in a patient, involves detecting nucleotide difference between patient
XX NSDHL oligonucleotide (gene encoding 3beta-hydroxysteroid dehydrogenase
XX (3beta-HSD)) and wild type NSDHL gene, or detecting accumulation of
XX sterol intermediates before the generation of cholest-8(9)-en-3beta-ol in
XX the cholesterol biosynthetic pathway, in the body fluids or cells of the
XX patient. The method is useful for diagnosing CHILD syndrome and psoriasis
XX in a patient. Other diseases implicated in defects of the cholesterol
XX biosynthetic pathway include mevalonic aciduria, desmosterolosis, Smith-
XX Lemli-Opitz syndrome (SLOS), Conradi-Hunermann-Happle syndrome;
XX chondroplasia punctata (X-linked disease), bone disorders, osteoporosis,
XX osteosclerosis, skin disorders, ichthyosis, eye disorders, cataracts,
XX and microphthalmia and arthritis. The human NSDHL gene is located on
XX chromosome X128. The present sequence is a primer for routine sequencing
XX of and mutation detection in the human NSDHL gene (one of 8 exons or the
XX non-coding region)
XX
XX
XX Sequence 20 BP; 8 A; 2 C; 7 G; 3 T; 0 U; 0 Other;
XX
XX
XX Query Match 66.7%; Score 12; DB 10; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 7.5e+03;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX
XX 3 CCCCTCTTCGG 14
XX |||||
XX |||||
XX |||||
XX
XX 20 CCCCTCTTCGG 9
XX

```

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 7, 2006, 08:39:24 ; Search time 105.568 Seconds

(without alignments)
303.087 Million cell updates/sec

Title: US-10-659-980A-5

Perfect score: 18
Sequence: 1 cccccctctctgataac 18

Scoring table: OLIGO-NC
Gapop 60.0 , Gapext 60.0

Searched: 1303057 seqs, 888780828 residues

Word size: 11

Total number of hits satisfying chosen parameters: 1026028

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Listing first 45 summaries

Database:

Issued Patents NA:
1: /cgn2_6/prodata/1/ina/1/COMB.seq:*
2: /cgn2_6/prodata/1/ina/5/COMB.seq:*
3: /cgn2_6/prodata/1/ina/6A/COMB.seq:*
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5: /cgn2_6/prodata/1/ina/H/COMB.seq:*
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8: /cgn2_6/prodata/1/ina/RE/COMB.seq:*
9: /cgn2_6/prodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	12	66.7	17	US-09-583-610D-17	Sequence 17, App1
2	12	66.7	20	US-08-173-489C-17	Sequence 17, App1
3	12	66.7	20	US-09-198-452A-2493	Sequence 2493, App
4	12	66.7	20	US-10-002-623-451	Sequence 451, App
5	12	66.7	25	US-09-396-196G-24325	Sequence 24325, A
6	11	61.1	15	US-09-094-714A-4	Sequence 4, App1
7	11	61.1	18	US-09-474-922A-14	Sequence 14, App1
8	11	61.1	20	US-09-280-799-154	Sequence 154, App1
9	11	61.1	20	US-09-277-020-18	Sequence 18, App1
10	11	61.1	20	US-09-060-299-126	Sequence 126, App
11	11	61.1	22	US-09-402-923A-126	Sequence 126, App
12	11	61.1	22	US-08-117-952-432	Sequence 432, App
13	11	61.1	22	US-10-341-199-18	Sequence 18, App1
14	11	61.1	25	US-08-538-875-24	Sequence 24, App1
15	11	61.1	25	US-09-142-355B-23	Sequence 23, App1
16	11	61.1	25	US-09-699-931-23	Sequence 10385, A
17	11	61.1	25	US-09-396-196G-10385	Sequence 10385, A
18	11	61.1	25	US-09-396-196G-10387	Sequence 10387, A
19	11	61.1	25	US-09-396-196G-10388	Sequence 10388, A
20	11	61.1	25	US-09-396-196G-10388	Sequence 10388, A
21	11	61.1	25	US-09-396-196G-19355	Sequence 19355, A
22	11	61.1	25	US-09-396-196G-37093	Sequence 37093, A
23	11	61.1	25	US-09-396-196G-37094	Sequence 37094, A
24	11	61.1	25	US-09-396-196G-52013	Sequence 52013, A

25	11	61.1	25	3	US-09-396-196G-52014	Sequence 52014, A
26	11	61.1	25	3	US-09-396-196G-52015	Sequence 52015, A
27	11	61.1	25	3	US-09-396-196G-52016	Sequence 52016, A
28	11	61.1	25	3	US-09-396-196G-52017	Sequence 52017, A
29	11	61.1	25	3	US-09-396-196G-52911	Sequence 52911, A
30	11	61.1	25	3	US-09-396-196G-62035	Sequence 62035, A
31	11	61.1	25	3	US-09-396-196G-66069	Sequence 66069, A
32	11	61.1	25	3	US-09-396-196G-84553	Sequence 84553, A
33	11	61.1	25	3	US-09-396-196G-84554	Sequence 84554, A
34	11	61.1	25	3	US-09-396-196G-84565	Sequence 84565, A
35	11	61.1	25	3	US-09-396-196G-86459	Sequence 86459, A
36	11	61.1	25	3	US-09-396-196G-100179	Sequence 100179, A
37	11	61.1	25	3	US-09-396-196G-100180	Sequence 100180, A
38	11	61.1	25	3	US-09-396-196G-103140	Sequence 103140, A
39	11	61.1	25	3	US-09-396-196G-103141	Sequence 103141, A
40	11	61.1	25	3	US-09-396-196G-117806	Sequence 117806, A
41	11	61.1	28	2	US-08-579-777A-4	Sequence 4, App1
42	10	55.6	15	2	US-08-311-486C-125	Sequence 125, App
43	10	55.6	15	2	US-08-311-486C-126	Sequence 126, App
44	10	55.6	15	2	US-08-311-486C-127	Sequence 127, App
45	10	55.6	15	3	US-08-929-856-58	Sequence 58, App1

ALIGNMENTS

```

RESULT 1
US-09-583-610D-17
; Sequence 17, Application US/09583610D
; Patent No. 6740735
; GENERAL INFORMATION:
; APPLICANT: Gianturco, S.H.
; APPLICANT: Bradley, W.A.
; TITLE OF INVENTION: DNA Encoding Human apob48R: A Monocyte-Macrophage
; TITLE OF INVENTION: Apolipoprotein B48 Receptor Gene and Protein
; FILE REFERENCE: D5880CIP
; CURRENT APPLICATION NUMBER: US/09/583, 610D
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: US 09/130,242
; PRIOR FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 22
; SEQ ID NO 17
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense primers were based on the 5'-end
; OTHER INFORMATION: sequence of the THP-1 (73 clone (bp 2203-2187
; OTHER INFORMATION: of Apob48R cDNA)
US-09-583-610D-17

Query Match          66.7%; Score 12; DB 3; Length 17;
Best local similarity 100.0%; Pred. No. 1e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      5 CCTCTCTTGAT 16
Db      5 CCTCTCTTGAT 16

RESULT 2
US-08-173-489C-17/c
; Sequence 17, Application US/08173489C
; Patent No. 5861244
; GENERAL INFORMATION:
; APPLICANT: WANG, C. -G.
; APPLICANT: HERBURN, A. G.
; TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
; NUMBER OF SEQUENCES: 365
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
; STREET: 510 EAST 73RD STREET,

```

CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10021.
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44mb storage
COMPUTER: IBM PC/XT/AT
OPERATING SYSTEM: MS-DOS version 6.2
SOFTWARE: Wordperfect Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 22 DEC 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/968,436
FILING DATE: 29 OCT 1992
ATTORNEY/AGENT INFORMATION:
NAME: Handelsman, Joseph H.
REGISTRATION NUMBER: 26,179
REFERENCE/DOCKET NUMBER: US518-6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (attorney) (212) 708-1880
TELEFAX: (attorney) (212) 246-8959
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
DESCRIPTION: n-myc gene (Accession # Y00664)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
AUTHORS: Ibeon, J M, Rabbits, P H.
TITLE: Sequence of a germ-line N-myc
Patent No. 5861244
TITLE: Gene and amplification as a mechanism of
activation
JOURNAL: Oncogene
VOLUME: 2
PAGES: 399-402
DATE: 1988
RELEVANT RESIDUES IN SEQ ID NO: 17 :FROM 1 TO 20
US-08-173-489C-17

Query Match 66.7%; Score 12; DB 2; Length 20;
Best Local Similarity 100.0%; Pred.No. 1.1e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCCCTTCT 12
|||
Db 18 CCCCCCTTCT 7

RESULT 3
US-09-198-452A-2493
Sequence 2493, Application US/09198452A
Patent No. 6559294
GENERAL INFORMATION:
APPLICANT: Griffiths, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 2493
LENGTH: 20

TYPE: DNA
ORGANISM: Chlamydia pneumoniae
US-09-198-452A-2493

Query Match 66.7%; Score 12; DB 3; Length 20;
Best Local Similarity 100.0%; Pred.No. 1.1e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCTCTTCTGAT 16
|||||
Db 4 CCTCTTCTGAT 15

RESULT 4
US-10-002-623-451
Sequence 451, Application US/10002623
Patent No. 6929911
GENERAL INFORMATION:
APPLICANT: OEFNER, PETER J.
TITLE OF INVENTION: A METHOD FOR DETERMINING GENETIC
TITLE OF INVENTION: APPLICATION, SUBSTRUCTURE AND GENE FLOW WITHIN HUMAN
TITLE OF INVENTION: POPULATIONS
FILE REFERENCE: STAN-212
CURRENT APPLICATION NUMBER: US/10/002,623
CURRENT FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: US 60/245,355
PRIOR FILING DATE: 2000-11-01
NUMBER OF SEQ ID NOS: 952
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 451
LENGTH: 20
TYPE: DNA
ORGANISM: Homo Sapiens
US-10-002-623-451

Query Match 66.7%; Score 12; DB 3; Length 20;
Best Local Similarity 100.0%; Pred.No. 1.1e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCCCCCTTCTG 13
|||||
Db 9 CCCCCCTTCTG 20

RESULT 5
US-09-396-196G-24325
Sequence 24325, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Miltmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 24325
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-09-396-196G-24325

Query Match 66.7%; Score 12; DB 3; Length 25;
Best Local Similarity 100.0%; Pred.No. 1.1e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCTCTTCTGGA 15

Db 3 CCCTCTCTGGA 14

RESULT 6
US-09-094-714A-4
Sequence 4, Application US/09094714A
Patent No. 6117847

GENERAL INFORMATION:

APPLICANT: C. Frank Bennett, Nicholas M. Dean

TITLE OF INVENTION: OLIGONUCLEOTIDES FOR ENHANCED MODULATION OF

TITLE OF INVENTION: PROTEIN KINASE C EXPRESSION

NUMBER OF SEQUENCES: 69

CORRESPONDENCE ADDRESS:

ADDRESS: Woodcock Washburn Kurtz Mackiewicz & No. 611784718, LLP

STREET: One Liberty Place - 46th Floor

CITY: Philadelphia

STATE: PA

COUNTRY: USA

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE

COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS

SOFTWARE: WORDPERFECT 8.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/094,714A

FILING DATE: June 15, 1998

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/601,269

FILING DATE: 14-FEB-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/478,178

FILING DATE: 07-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/089,996

FILING DATE: 09-JUL-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/852,852

FILING DATE: 16-MAR-1992

ATTORNEY/AGENT INFORMATION:

NAME: Paul K. Legaard

REGISTRATION NUMBER: 38,534

REFERENCE/DOCKET NUMBER: ISIS-2943

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-3100

TELEFAX: (215) 568-3439

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 15

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-09-094-714A-4

Query Match 61.1%; Score 11; DB 3; Length 15;

Best Local Similarity 100.0%; Pred. No. 3.7e+03;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCCTCTCTCT 12

Db 2 CCCTCTCTCT 12

RESULT 7

US-09-474-922A-14

Sequence 14, Application US/09474922A

Patent No. 6187586

GENERAL INFORMATION:

APPLICANT: Brett P. Monia

APPLICANT: Lex M. Cowsett

APPLICANT: Richard A. Roth

TITLE OF INVENTION: ANTISENSE MODULATION OF Akt-3 EXPRESSION

FILE REFERENCE: RTS-0036

CURRENT APPLICATION NUMBER: US/09/474,922A

CURRENT FILING DATE: 1999-12-29

NUMBER OF SEQ ID NOS: 89

SEQ ID NO 14

LENGTH: 18

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Antisense Oligonucleotide

US-09-474-922A-14

Query Match 61.1%; Score 11; DB 3; Length 18;

Best Local Similarity 100.0%; Pred. No. 3.7e+03;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCTCTCTG 13

Db 2 CCCTCTCTG 12

RESULT 8

US-09-280-799-154

Sequence 154, Application US/09280799

Patent No. 6136603

GENERAL INFORMATION:

APPLICANT: Dean, Nicholas M.

APPLICANT: Karrera, James G

APPLICANT: McKay, Robert

TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN-5 SIGNAL

TITLE OF INVENTION: TRANSDUCTION

FILE REFERENCE: ISPH-0340

CURRENT APPLICATION NUMBER: US/09/280,799

CURRENT FILING DATE: 1999-03-26

NUMBER OF SEQ ID NOS: 208

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 154

LENGTH: 20

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-09-280-799-154

Query Match 61.1%; Score 11; DB 3; Length 20;

Best Local Similarity 100.0%; Pred. No. 3.8e+03;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCCTCTCTGG 14

Db 10 CCCTCTCTGG 20

RESULT 9

US-09-277-020-18

Sequence 18, Application US/09277020

Patent No. 6210892

GENERAL INFORMATION:

APPLICANT: Bennett, C. Frank

TITLE OF INVENTION: Alteration of Cellular Behavior by Antisense Modulation

FILE REFERENCE: ISPH-0339

CURRENT APPLICATION NUMBER: US/09/277,020

CURRENT FILING DATE: 1999-03-26

EARLIER APPLICATION NUMBER: 09/167,921

EARLIER FILING DATE: 1998-10-07

NUMBER OF SEQ ID NOS: 65

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 18

LENGTH: 20

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-277-020-18

Query Match 61.1%; Score 11; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCTCTTCTGG 14
|||||
Db 10 CCTCTTCTGG 20

RESULT 10
US-09-060-299-126
Sequence 126, Application US/09060299
Patent No. 6545137
GENERAL INFORMATION:
APPLICANT: Todd, John A
APPLICANT: Hees, John W
APPLICANT: Caskey, Charles T
APPLICANT: Cox, Roger D
APPLICANT: Gerhold, David
APPLICANT: Hammond, Holly
APPLICANT: Hey, Patricia
APPLICANT: Kawaguchi, Yoshihiko
APPLICANT: Metzger, Tony R
APPLICANT: Merriman, Michael L
TITLE OF INVENTION: No. 6545137el Receptor
NUMBER OF SEQUENCES: 455
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon and Vanderhye
STREET: 1100 No. 6545137th Glebe Road, Eighth Floor
CITY: Arlington
STATE: Virginia
COUNTRY: US
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/060,299
FILING DATE: 15-APR-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/043,553
FILING DATE: 15-APR-1997
PRIOR APPLICATION DATA: US 60/048,740
APPLICATION NUMBER: US 60/048,740
FILING DATE: 05-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: B.J.Sadoff
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 620-35
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4091
TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 126:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-060-299-126

Query Match 61.1%; Score 11; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCTCTTCTGA 15
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Db 8 CCTCTTCTGA 18

RESULT 11
US-09-402-923A-126
Sequence 126, Application US/09402923A
Patent No. 6555654
GENERAL INFORMATION:
APPLICANT: Todd, John A
APPLICANT: Hees, John W
APPLICANT: Caskey, Charles T
APPLICANT: Cox, Roger D
APPLICANT: Gerhold, David
APPLICANT: Hammond, Holly
APPLICANT: Hey, Patricia
APPLICANT: Kawaguchi, Yoshihiko
APPLICANT: Metzger, Tony R
APPLICANT: Merriman, Michael L

TITLE OF INVENTION: No. 6555654el LDL-Receptor
NUMBER OF SEQUENCES: 455
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon and Vanderhye
STREET: 1100 No. 6555654th Glebe Road, Eighth Floor
CITY: Arlington
STATE: Virginia
COUNTRY: US
ZIP: VA 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/402,923A
FILING DATE: 14-Feb-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB98/01102
FILING DATE: 15-APR-1998
APPLICATION NUMBER: US 60/043,553
FILING DATE: 15-APR-1997
APPLICATION NUMBER: US 60/048,740
FILING DATE: 05-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: B.J.Sadoff
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 620-81
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4091
TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 126:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 126:
US-09-402-923A-126

Query Match 61.1%; Score 11; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCTCTTCTGA 15
|||||
Db 8 CCTCTTCTGA 18

RESULT 12
US-08-117-952-432/c
Sequence 432, Application US/08117952
Patent No. 5851760
GENERAL INFORMATION:
APPLICANT: Evans, Glen A.
APPLICANT: Smith, Michael W.

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; TITLE OF INVENTION: METHOD FOR GENERATION OF SEQUENCE
; TITLE OF INVENTION: SAMPLED MAPS OF COMPLEX GENOMES
; NUMBER OF SEQUENCES: 797
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jprety, Schroeder, Brueggemann & Clark
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/117,952
; FILING DATE: 07-SEP-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/078,471
; FILING DATE: 15-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen B.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9423
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-546-4737
; TELEFAX: 619-546-9392
; INFORMATION FOR SEQ ID NO: 432:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Oligonucleotide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; US-08-117-952-432

Query Match      61.1%; Score 11; DB 2; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 CCTCTTCTGCA 15
DB      14 CCTCTTCTGCA 4

RESULT 13
US-10-341-199-18/c
; Sequence 18, Application US/10341199
; Patent No. 6852494
; GENERAL INFORMATION:
; APPLICANT: Liao, Halsun
; APPLICANT: Deik, Amy Anderson
; APPLICANT: Mamaeva, Natalia
; APPLICANT: Woodward, Caroline Ngaara
; APPLICANT: Chen, Shin-Yih
; APPLICANT: Huang, Yih
; APPLICANT: Shen, Ming
; APPLICANT: Law, Simon W.
; APPLICANT: Huang, Tai-Neng
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION
; FILE REFERENCE: 12251-036001
; CURRENT APPLICATION NUMBER: US/10/341,199
; CURRENT FILING DATE: 2003-01-10
; NUMBER OF SEQ. ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
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; FEATURE:
; OTHER INFORMATION: Synthetically generated oligonucleotide
; US-10-341-199-18

Query Match      61.1%; Score 11; DB 3; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CCCCCTCTTCT 12
DB      11 CCCCCTCTTCT 1

RESULT 14
US-08-538-875-24/c
; Sequence 24, Application US/08538875
; Patent No. 5773582
; GENERAL INFORMATION:
; APPLICANT: Shin, Hang-Cheol
; APPLICANT: Shin, Nam-Kyu
; APPLICANT: Lee, Inkyung
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR MUTAINS
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Shin, Hang-Cheol
; STREET: Jukong Gocheung Apt. 1014-806, Haan-dong
; CITY: Kwangmyung-shi
; STATE: Kyungki-do
; COUNTRY: Republic of Korea
; ZIP: 423-060
; ADDRESSEE: Shin, Nam-Kyu
; STREET: #181-404 Sadang-4-dong, Dongjak-ku
; CITY: Seoul
; STATE:
; COUNTRY: Republic of Korea
; ZIP: 156-094
; ADDRESSEE: Lee, Inkyung
; STREET: 11/2, #302-39 Jnan-4-dong, Nam-ku
; CITY: Incheon
; STATE:
; COUNTRY: Republic of Korea
; ZIP: 402-204
; ADDRESSEE: Kang, Sungzong
; STREET: #84-4 Daeshin-dong, Seodaemun-ku
; CITY: Seoul
; STATE:
; COUNTRY: Republic of Korea
; ZIP: 120-160
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette 3.5inch 2.0Mb storage
; COMPUTER: IBM PC/AT
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/538,875
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/193,336
; FILING DATE:
; APPLICATION NUMBER: KR 93-1751
; FILING DATE: 9-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX:
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 bases
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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: primer DNA
US-08-538-875-24

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Query Match      61.1%; Score 11; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      4  CCCCTCTCTG 14
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Db       16  CCCCTCTCTG 6

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RESULT 15
US-09-142-355B-23/c
; Sequence 23; Application US/09142355B
; Patent No. 6184012
; GENERAL INFORMATION:
; APPLICANT: Neri, Dario
; APPLICANT: Demartis, Salvatore
; APPLICANT: Huber, Adrain
; APPLICANT: Viti, Francesca
; APPLICANT: Tawfik, Dan. S.
; APPLICANT: Winter, Gregory Paul
; TITLE OF INVENTION: Isolation of Enzymes
; FILE REFERENCE: 2224/08665
; CURRENT APPLICATION NUMBER: US/09/142,355B
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: GB 9608540.2
; PRIOR FILING DATE: 1996-04-25
; PRIOR APPLICATION NUMBER: PCT/GB97/01153
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-09-142-355B-23

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Query Match      61.1%; Score 11; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      8  CTTCTGATAC 18
         |||||
Db       20  CTTCTGATAC 10

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Search completed: April 7, 2006, 17:01:17
 Job time : 106.568 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 7, 2006, 08:39:19 ; Search time 923.838 Seconds
(without alignments)
1107.534 Million cell updates/sec

Title: US-10-659-980A-5

Perfect score: 18
Sequence: 1 cccccctctctgcatc 18

Scoring table: OH160A100

Gapop 60.0 , Gapext 60.0

Searched: 5883141 seqs, 28421725653 residues

Word size: 17

Total number of hits satisfying chosen parameters: 1640572

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Listing first 45 summaries

Database : GenEmbl:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	6	CQ796912 Sequence
2	18	100.0	18	6	CS089158 Sequence
3	18	100.0	18	6	AX316096 Sequence
4	14	77.8	18	6	CS089171 Sequence
5	14	77.8	18	6	AX316109 Sequence
6	12	66.7	17	6	AR568743 Sequence
7	12	66.7	17	6	AX727540 Sequence
8	12	66.7	17	6	AX733930 Sequence
9	12	66.7	17	6	AX760134 Sequence
10	12	66.7	18	6	CQ796913 Sequence
11	12	66.7	18	6	CS089159 Sequence
12	12	66.7	18	6	AX316097 Sequence
13	12	66.7	18	8	HERETRO11
14	12	66.7	19	6	AX112294 Sequence
15	12	66.7	20	6	AR029828 Sequence
16	12	66.7	20	6	AR311956 Sequence
17	12	66.7	20	6	AX298879 Sequence
18	12	66.7	25	6	AX112272 Sequence

19	11	61.1	17	6	AX722644	Sequence
20	11	61.1	17	6	AX723024	Sequence
21	11	61.1	17	6	AX724707	Sequence
22	11	61.1	17	6	AX726733	Sequence
23	11	61.1	18	6	AR130022	Sequence
24	11	61.1	18	6	BD102009	Agonist a
25	11	61.1	18	6	BD102163	Apoptosis
26	11	61.1	18	6	BD169223	Degraded
27	11	61.1	18	6	BD169334	Small rem
28	11	61.1	19	6	AX299005	Sequence
29	11	61.1	20	6	AR136351	Sequence
30	11	61.1	20	6	AR144290	Sequence
31	11	61.1	20	6	BD106083	Novel LDL
32	11	61.1	20	6	BD247806	Antisense
33	11	61.1	20	6	AR305172	Sequence
34	11	61.1	20	6	AR309276	Sequence
35	11	61.1	20	6	AX826876	Sequence
36	11	61.1	21	6	CS064811	Sequence
37	11	61.1	21	6	CS088202	Sequence
38	11	61.1	22	6	AR067084	Sequence
39	11	61.1	22	6	AR634906	Sequence
40	11	61.1	23	6	CQ888258	Sequence
41	11	61.1	25	6	A67134	Sequence 23
42	11	61.1	25	6	AR014476	Sequence
43	11	61.1	25	6	AR267420	Sequence
44	11	61.1	27	6	AX117396	Sequence
45	11	61.1	28	6	AR071893	Sequence

ALIGNMENTS

RESULT 1	CQ796912	18 bp	DNA	linear	PAT 19-APR-2004
LOCUS	CQ796912	Sequence 5 from Patent WO2004026772.			
DEFINITION	CQ796912				
ACCESSION	CQ796912.1	GI:46408538			
VERSION					
KEYWORDS					
SOURCE					
ORGANISM					
synthetic construct					
other sequences; artificial sequences.					
REFERENCE					
1	Hovane, T.A.				
Ammunite-oxidizing bacteria and methods of using and detecting					
thesame					
Patent: WO 2004026772-A 5 01-APR-2004;					
Aquaria Inc. (US)					
FEATURES					
source					
1..18					
/organism="synthetic construct"					
/mol_type="unassigned DNA"					
/db_xref="taxon:32630"					
/note="Oligonucleotide probe"					
ORIGIN					
Query Match	100.0%	Score 18;	DB 6;	Length 18;	
Best Local Similarity	100.0%;	Pred. No. 10;			
Matches	18;	Conservative	0;	Mismatches	0;
Indels	0;	Gaps	0;		
QY	1	CCCCCTCTCTCGATAC	18		
DB	1	CCCCCTCTCTCGATAC	18		
RESULT 2	CS089158	18 bp	DNA	linear	PAT 25-MAY-2005
LOCUS	CS089158	Sequence 5 from Patent EP1502948.			
DEFINITION	CS089158				
ACCESSION	CS089158.1	GI:6674442			
VERSION					
KEYWORDS					
SOURCE					
synthetic construct					

ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE
1
AUTHORS Hovanec, T.A. and Burrell, P.C.
TITLE Ammonia-oxidizing bacteria
JOURNAL Patent: EP 1502948-A 5 02-FEB-2005;
AquaRIA Inc. (US)
FEATURES Location/Qualifiers
source 1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Description of Artificial Sequence: Probe"

ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCCCTTCTTGATAC 18
1 CCCCCCTTCTTGATAC 18

Db 1 CCCCCCTTCTTGATAC 18

RESULT 3
AX316096 18 bp DNA linear PAT 14-DEC-2001
LOCUS
DEFINITION Sequence 5 from Patent WO0190312.
ACCESSION AX316096
VERSION AX316096.1 GI:17899287
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE
1
AUTHORS Hovanec, T.A. and Burrell, P.C.
TITLE Ammonia-oxidizing bacteria
JOURNAL Patent: WO 0190312-A 5 29-NOV-2001;
AquaRIA, INC. (US)
FEATURES Location/Qualifiers
source 1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Probe"

ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCCCTTCTTGATAC 18
1 CCCCCCTTCTTGATAC 18

Db 1 CCCCCCTTCTTGATAC 18

RESULT 4
CS089171 18 bp DNA linear PAT 25-MAY-2005
LOCUS
DEFINITION Sequence 18 from Patent EP1502948.
ACCESSION CS089171
VERSION CS089171.1 GI:66714455
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE
1
AUTHORS Hovanec, T.A. and Burrell, P.C.
TITLE Ammonia-oxidizing bacteria
JOURNAL Patent: EP 1502948-A 18 02-FEB-2005;
AquaRIA Inc. (US)
FEATURES Location/Qualifiers
source 1..18

/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Description of Artificial Sequence: Primer"

ORIGIN

Query Match 77.8%; Score 14; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCCCTTCTTGG 14
1 CCCCCCTTCTTGG 14

Db 1 CCCCCCTTCTTGG 14

RESULT 5
AX316109 18 bp DNA linear PAT 14-DEC-2001
LOCUS
DEFINITION Sequence 18 from Patent WO0190312.
ACCESSION AX316109
VERSION AX316109.1 GI:17899300
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE
1
AUTHORS Hovanec, T.A. and Burrell, P.C.
TITLE Ammonia-oxidizing bacteria
JOURNAL Patent: WO 0190312-A 18 29-NOV-2001;
AquaRIA, INC. (US)
FEATURES Location/Qualifiers
source 1..18
/organism="synthetic construct"
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/db_xref="taxon:32630"
/note="Primer"

ORIGIN

Query Match 77.8%; Score 14; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCCCTTCTTGG 14
1 CCCCCCTTCTTGG 14

Db 1 CCCCCCTTCTTGG 14

RESULT 6
AR568743 17 bp DNA linear PAT 14-DEC-2004
LOCUS
DEFINITION Sequence 17 from patent US 6740735.
ACCESSION AR568743
VERSION AR568743.1 GI:56568296
KEYWORDS
SOURCE unknown.
ORGANISM unknown.
unclassified.

REFERENCE
1 (bases 1 to 17)
AUTHORS Gianturco, S.H. and Bradley, W.A.
TITLE DNA encoding human apob48r: a monocyte-macrophage apolipoprotein
JOURNAL B48 receptor gene and protein
Patent: US 6740735-A 17 25-MAY-2004;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 66.7%; Score 12; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.9e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CCTCTTCTGAT 16

ACCESSION	CS089159		GI:66714443	
VERSION	CS089159.1			
KEYWORDS				
SOURCE				
ORGANISM				
REFERENCE				
AUTHORS	Hovanec,T.A. and Burrell,P.C.			
TITLE	Ammonia-oxidizing bacteria			
JOURNAL	Patent: EP 1502948-A 6 02-FEB-2005;			
	Aquaria Inc. (US)			
FEATURES				
source	1..18			
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	/db_xref="taxon:32630"			
	/note="Description of Artificial Sequence: Primer"			
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Query Match	66.7%; Score 12; DB 6; Length 18;			
Best Local Similarity	100.0%; Pred.No. 2.9e+04;			
Matches	12; Conservative 0; Mismatches 0; Gaps 0;			
OY	7 TCTTGTGATAC 18			
	18 TCTTGTGATAC 7			
RESULT 12				
LOCUS	AXJ16097	18 bp	DNA	linear
DEFINITION	Sequence 6 from Patent WO0190312.			PAT 14-DEC-2001
ACCESSION	AXJ16097			
VERSION	AXJ16097.1	GI:17899288		
KEYWORDS				
SOURCE				
ORGANISM				
REFERENCE				
AUTHORS	Hovanec,T.A. and Burrell,P.C.			
TITLE	Ammonia-oxidizing bacteria			
JOURNAL	Patent: WO 0190312-A 6 29-NOV-2001;			
	AQUARIA INC. (US)			
FEATURES				
source	1..18			
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	/mol_type="unassigned DNA"			
	/db_xref="taxon:32630"			
	/note="Primer"			
ORIGIN				
Query Match	66.7%; Score 12; DB 6; Length 18;			
Best Local Similarity	100.0%; Pred.No. 2.9e+04;			
Matches	12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
OY	7 TCTTGTGATAC 18			
	18 TCTTGTGATAC 7			
Db				
RESULT 13				
LOCUS	HSRRTPO11	18 bp	DNA	linear
DEFINITION	H.sapiens Ret Proto-Oncogene, Intron 11 (3').			PRI 13-DEC-1994
ACCESSION	X79751			
KEYWORDS	K79751.1 GI:601962			
SOURCE	Intron; ret gene; ret proto-oncogene.			
ORGANISM	Homo sapiens (human)			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;			
	Homnidae; Homo.			
REFERENCE				
	1			

AUTHORS	Mulligan, L.M., Eng, C., Attie, T., Lyons, S., Marsh, D.J., Hyland, V.J., Robinson, B.G., Fritling, A., Verellen-Dumoulin, C., Satai, A., Venter, D.J., Munich, A., and Funder, B.A.J. Diverse phenotypes associated with exon 10 mutations of the RET proto-oncogene Hum. Mol. Genet. 3 (12), 2163-2167 (1994)									
JOURNAL	2 (bases 1 to 18)									
REFERENCE	Eng, C. Direct Submission Submitted (14-JUN-1994) C. Eng, University of Cambridge, Dept of Pathology, Tennis Court Road, Cambridge CB2 1QP, UK									
AUTHORS	location/Qualifiers									
JOURNAL	1. .18									
FEATURES	/organism="Homo sapiens"									
SOURCE	/mol_type="genomic DNA"									
	/isolate="CR3"									
	/db_xref="taxon:9606"									
	/chromosome="10"									
	/map="q11.2"									
	/germline									
gene	1. .18									
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intron	<1. .18									
	/gene="RET"									
	/note="3' end"									
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ORIGIN										
Query Match	66.7%; Score 12; DB 6; Length 19;									
Best Local Similarity	100.0%; Pred. No. 2.9e+04;									
Matches	12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1 CCCCCCTTCT 12									
Db	6 CCCCCCTTCT 17									
RESULT 14										
AX112294/C	19 bp DNA linear PAT 01-MAY-2001									
LOCUS	AX112294									
DEFINITION	Sequence 23 from Patent WO0127304.									
ACCESSION	AX112294									
VERSION	AX112294.1 GI:13939098									
KEYWORDS	.									
SOURCE	synthetic construct									
ORGANISM	synthetic construct									
REFERENCE	other sequences; artificial sequences.									
AUTHORS	1									
	Charneau, P., Zennou, V., Pelumbo, F., Sirven, A. and Dubart Kupperschmitt, A. Lentiviral triplex dna, and vectors and recombinant cells containing lentiviral triplex dna Patent: WO 0127304-A 23 15-APR-2001.									
JOURNAL	INSTITUT PASTEUR (FR) ; INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE (INSERM) (FR)									
FEATURES	location/Qualifiers									
SOURCE	1. .19									
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	/mol_type="unassigned DNA"									
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ORIGIN										
Query Match	66.7%; Score 12; DB 6; Length 19;									
Best Local Similarity	100.0%; Pred. No. 2.9e+04;									
Matches	12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1 CCCCCCTTCT 12									
Db	19 CCCCCCTTCT 8									

RESULT 15

AR029828/c

LOCUS AR029828 20 bp DNA linear PAT 29-SEP-1999

DEFINITION Sequence 17 from patent US 5861244.

ACCESSION AR029828

VERSION AR029828.1 GI:5943042

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

ORIGIN

Query Match

Best Local Similarity

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCCCTCTCT 12

DB 18 CCCCCCTCTCT 7

Search completed: April 7, 2006, 09:11:08

Job time : 925.838 secs

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OM nucleic - nucleic search, using sw model

Run on: April 7, 2006, 08:38:29 ; Search time 780.324 Seconds

(without alignments)
92.282 Million cell updates/sec

Title: US-10-659-980A-5

Perfect score: 18

Sequence: 1 ccccccctcttcgcatc 18

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Gapop 10.0, Gapext 1.0

Searched: 9267905 seqs, 2000278028 residues

Total number of hits satisfying chosen parameters: 13050014

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Database: Published Applications NA New:

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15: /SIDS/prodata/1/pubpna/US60_NEW_PUB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	13.8	76.7	19	US-11-101-244-1578545
4	13.8	76.7	19	US-11-083-784-1578545
5	13.8	76.7	25	US-11-121-849-325987
6	13.8	76.7	25	US-11-136-527-352597
7	13.8	76.7	25	US-11-136-527-352597
8	13.8	76.7	25	US-11-136-527-352597
9	13.4	74.4	21	US-10-310-914A-908031
10	13.4	74.4	24	US-10-310-914A-84927
11	13.4	74.4	25	US-11-121-849-394245
12	13.2	73.3	19	US-10-310-914A-1353078
13	13.2	73.3	19	US-11-101-244-1473850
14	13.2	73.3	19	US-11-083-784-1473850
15	13.2	73.3	21	US-10-770-726-11899
16	13.2	73.3	21	US-10-310-914A-896978
17	13.2	73.3	22	US-10-310-914A-691838
18	13.2	73.3	22	US-10-310-914A-691951

19	13.2	73.3	24	US-10-310-914A-447953	Sequence 447953,
20	13.2	73.3	25	US-10-310-914A-935287	Sequence 935287,
21	13.2	73.3	25	US-10-310-914A-967300	Sequence 967300,
22	13.2	73.3	25	US-10-933-982-9664	Sequence 9664, A
23	13.2	73.3	25	US-11-121-849-36513	Sequence 36513, A
24	13.2	73.3	25	US-11-121-849-171065	Sequence 171065,
25	13.2	73.3	25	US-11-121-849-177842	Sequence 377842,
26	13.2	73.3	30	US-11-170-751-2	Sequence 2,
27	13	72.2	19	US-11-101-244-1230837	Sequence 1230837,
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29	13	72.2	23	US-10-310-914A-224598	Sequence 224598,
30	13	72.2	25	US-10-934-048A-68320	Sequence 68320, A
31	13	72.2	27	US-10-310-914A-224598	Sequence 224598,
32	12.8	71.1	18	US-10-310-914A-896977	Sequence 896977,
33	12.8	71.1	20	US-11-111-288-234	Sequence 234, App
34	12.8	71.1	21	US-10-310-914A-447881	Sequence 447881,
35	12.8	71.1	21	US-10-310-914A-1261081	Sequence 1261081,
36	12.8	71.1	22	US-10-310-914A-466300	Sequence 466300,
37	12.8	71.1	22	US-10-310-914A-899298	Sequence 899298,
38	12.8	71.1	22	US-10-310-914A-1261104	Sequence 1261104,
39	12.8	71.1	23	US-10-310-914A-764601	Sequence 764601,
40	12.8	71.1	23	US-10-310-914A-830964	Sequence 830964,
41	12.8	71.1	23	US-10-310-914A-1109455	Sequence 1109455,
42	12.8	71.1	25	US-10-310-914A-1109461	Sequence 1109461,
43	12.8	71.1	25	US-10-932-182A-70617	Sequence 70617, A
44	12.8	71.1	25	US-10-932-182A-70617	Sequence 70617, A
45	12.8	71.1	25	US-11-121-849-36514	Sequence 36514, A

ALIGNMENTS

RESULT 1
US-10-310-914A-1061199/c
Sequence 1061199, Application US/10310914A
Publication No. US2006000322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
TITLE OF INVENTION: Biointernationally detectable group of novel regulatory genes an
FILE REFERENCE: 06087, 0200, CPUS01
CURRENT APPLICATION NUMBER: US/10/310, 914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1061199
LENGTH: 25
TYPE: RNA
ORGANISM: Human
US-10-310-914A-1061199

Query Match 77.8%; Score 14; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CCCCCTCTTCGGA 15
Db 20 CCCCCTCTTCGGA 7

RESULT 2
US-11-121-849-112898
Sequence 112898, Application US/11121849
Publication No. US20050272080A1
GENERAL INFORMATION:
APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121, 849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567, 949

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/ PRIOR FILING DATE: 2004-05-03
/ NUMBER OF SEQ ID NOS: 673904
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 112898
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-11-121-849-112898
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Query Match 77.8%; Score 14; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 4 CCGCTCTCTGATA 17
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Db 6 CCGCTCTCTGATA 19
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RESULT 3
US-11-101-244-1578545
/ Sequence 1578545, Application US/11101244
/ Publication No. US20050246794A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 134990S
/ CURRENT APPLICATION NUMBER: US/11/101,244
/ PRIOR FILING DATE: 2005-04-07
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 1578545
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-101-244-1578545
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Query Match 76.7%; Score 13.8; DB 12; Length 19;
Best Local Similarity 64.7%; Pred. No. 8.5e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
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Qy 1 CCCCCCTCTCTGATA 17
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Db 1 CCACCTUCUCUGAUA 17
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RESULT 4
US-11-083-784-1578545
/ Sequence 1578545, Application US/11083784
/ Publication No. US20050245475A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 134990S
/ CURRENT APPLICATION NUMBER: US/11/083,784
/ PRIOR FILING DATE: 2005-03-18
/ PRIOR APPLICATION NUMBER: US/10/714,333
/ PRIOR FILING DATE: 2003-11-14
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
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/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 1578545
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-083-784-1578545
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Query Match 76.7%; Score 13.8; DB 13; Length 19;
Best Local Similarity 64.7%; Pred. No. 8.5e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
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Qy 1 CCCCCCTCTCTGATA 17
|||
Db 1 CCACCTUCUCUGAUA 17
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RESULT 5
US-11-121-849-325988
/ Sequence 325988, Application US/11121849
/ Publication No. US20050272080A1
/ GENERAL INFORMATION:
/ APPLICANT: John Palma
/ TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
/ FILE REFERENCE: 3684.1
/ CURRENT APPLICATION NUMBER: US/11/121,849
/ PRIOR FILING DATE: 2005-05-03
/ PRIOR APPLICATION NUMBER: 60/567,949
/ PRIOR FILING DATE: 2004-05-03
/ NUMBER OF SEQ ID NOS: 673904
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 325988
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-11-121-849-325988
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Query Match 76.7%; Score 13.8; DB 14; Length 25;
Best Local Similarity 88.2%; Pred. No. 9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Db 7 CCGCCCTCTCTGAGA 23
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RESULT 6
US-11-136-527-352597/c
/ Sequence 352597, Application US/11136527
/ Publication No. US20050287570A1
/ GENERAL INFORMATION:
/ APPLICANT: Wyeth
/ APPLICANT: Mount, William M
/ TITLE OF INVENTION: Probe Arrays for Expression Profiling of Rat Genes
/ FILE REFERENCE: 031896-041000 (AM101086)
/ CURRENT APPLICATION NUMBER: US/11/136,527
/ CURRENT FILING DATE: 2005-05-25
/ PRIOR APPLICATION NUMBER: US 60/574,294
/ PRIOR FILING DATE: 2005-05-26
/ NUMBER OF SEQ ID NOS: 362830
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 352597
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Probe
US-11-136-527-352597
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Query Match 76.7%; Score 13.8; DB 14; Length 25;
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Best Local Similarity 88.2%; Pred. No. 9e+02; Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCCCCCTTCTGGATAC 18
DB 22 CCACCTCGCTGGATAC 6

RESULT 7

US-11-136-527-352621/c
; Sequence 352621, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; PRIOR FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 352621
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Probe
US-11-136-527-352621

Query Match
Best Local Similarity 88.2%; Pred. No. 9e+02; Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCCCCCTTCTGGATAC 18
DB 19 CCACCTCGCTGGATAC 3

RESULT 8

US-11-136-527-352632/c
; Sequence 352632, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; PRIOR FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 352632
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Probe
US-11-136-527-352632

Query Match
Best Local Similarity 88.2%; Pred. No. 9e+02; Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCCCCCTTCTGGATAC 18
DB 17 CCACCTCGCTGGATAC 1

RESULT 9

US-10-310-914A-908031/c
; Sequence 908031, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes an

; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; PRIOR FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 908031
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-908031

Query Match
Best Local Similarity 93.3%; Pred. No. 1.4e+03; Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCCCCCTTCTGGA 15
DB 17 CCACCTCTTCTGGA 3

RESULT 10

US-10-310-914A-84927
; Sequence 84927, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes an
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; PRIOR FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 84927
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-84927

Query Match
Best Local Similarity 74.4%; Pred. No. 1.5e+03; Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCCCCCTTCTGGA 15
DB 6 CCCCCCTTCTGGA 20

RESULT 11

US-11-121-849-394245/c
; Sequence 394245, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; PRIOR FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 394245

LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-394245

Query Match 74.4%; Score 13.4; DB 14; Length 25;
Best Local Similarity 93.3%; Pred. No. 1.5e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 CCCCCTCTTGATGATA 17
DB 24 CCGCTCTTGATGATA 10

RESULT 12
US-10-310-914A-1353078/c
Sequence 1353078, Application US/10310914A
Publication No. US2006003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shlier, Kiyazac
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1353078
LENGTH: 19
TYPE: RNA
ORGANISM: Human
US-10-310-914A-1353078

Query Match 73.3%; Score 13.2; DB 8; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 CCCCCTCTCTGATAC 18
DB 19 CCGCCTCTCTGCTTAC 2

RESULT 13
US-11-101-244-1473850
Sequence 1473850, Application US/11101244
Publication No. US20050246794A1
GENERAL INFORMATION:
APPLICANT: Dharmoon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1473850
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-101-244-1473850

Query Match 73.3%; Score 13.2; DB 12; Length 19;
Best Local Similarity 61.1%; Pred. No. 1.8e+03;
Matches 11; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 1 CCCCCTCTCTGATAC 18
DB 2 CACCCACUUCUGUAGAC 19

RESULT 14
US-11-083-784-1473850
Sequence 1473850, Application US/11083784
Publication No. US20050245475A1
GENERAL INFORMATION:
APPLICANT: Dharmoon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1473850
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-083-784-1473850

Query Match 73.3%; Score 13.2; DB 13; Length 19;
Best Local Similarity 61.1%; Pred. No. 1.8e+03;
Matches 11; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 1 CCCCCTCTCTGATAC 18
DB 2 CACCCACUUCUGUAGAC 19

RESULT 15
US-10-770-726-11899/c
Sequence 11899, Application US/10770726
Publication No. US20050266409A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Brown, Eugene
APPLICANT: Liu, Wei
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
FILE REFERENCE: AM101079 (031896-010000)
CURRENT APPLICATION NUMBER: US/10/770,726
CURRENT FILING DATE: 2004-02-04
NUMBER OF SEQ ID NOS: 48640
SOFTWARE: PatentIn version 3.2
SEQ ID NO 11899
LENGTH: 21
TYPE: RNA
ORGANISM: RNA1
US-10-770-726-11899

Query Match 73.3%; Score 13.2; DB 8; Length 21;
Best Local Similarity 83.3%; Pred. No. 1.9e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 CCCCCTCTCTGATAC 18
DB 20 CCGCTCTCTGACAC 3

Mon Apr 10 08:45:42 2006

us-10-659-980a-5.sz30.rnpbn

Page 5

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Title: US-10-659-980A-5
Perfect score: 18
Sequence: 1 cccccctctcgatc 18

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	US-10-659-948A-5	Sequence 5, Appl1
2	18	100.0	18	US-10-659-980A-5	Sequence 5, Appl1
3	18	100.0	18	US-10-659-983A-5	Sequence 5, Appl1
4	14.4	80.0	25	US-10-719-956-558629	Sequence 558629,
5	14.4	80.0	30	US-09-320-337-74	Sequence 74, Appl
6	13.8	76.7	18	US-10-659-948A-21	Sequence 21, Appl
7	13.8	76.7	18	US-10-659-980A-21	Sequence 21, Appl
8	13.8	76.7	18	US-10-659-983A-21	Sequence 21, Appl
9	13.8	76.7	25	US-10-719-956-5535	Sequence 2535, A
10	13.8	76.7	25	US-10-719-956-50560	Sequence 50560, A
11	13.8	76.7	28	US-10-169-368-13	Sequence 13, Appl
12	13.4	74.4	25	US-10-719-956-94288	Sequence 94288, A
13	13.4	74.4	25	US-10-719-956-470164	Sequence 470164,
14	13.4	74.4	25	US-10-719-900-338352	Sequence 338352,
15	13.4	74.4	25	US-10-809-189-416880	Sequence 416880,
16	13.4	74.4	25	US-10-809-189-81113	Sequence 81113, A
17	13.4	74.4	25	US-11-060-756-202014	Sequence 202014,
18	13.4	74.4	25	US-11-060-756-286165	Sequence 286165,
19	13.2	73.3	20	US-10-492-928A-288	Sequence 288, App
20	13.2	73.3	25	US-10-719-956-650676	Sequence 650676,
21	13.2	73.3	25	US-10-719-900-84801	Sequence 84801, A
22	13.2	73.3	27	US-10-921-590-113	Sequence 113, App
23	13.2	73.3	28	US-10-492-928A-282	Sequence 282, App

C 24	13.2	73.3	30	7	US-10-282-122A-78603	Sequence 78603, A
C 25	13	72.2	25	7	US-10-719-956-117959	Sequence 117959,
C 26	13	72.2	25	7	US-10-719-956-193006	Sequence 193006,
27	13	72.2	25	7	US-10-719-956-511003	Sequence 511003,
28	13	72.2	25	7	US-10-719-956-611802	Sequence 611802,
29	13	72.2	25	8	US-10-719-900-316050	Sequence 316050,
30	13	72.2	25	8	US-10-719-900-574815	Sequence 574815,
C 31	13	72.2	25	10	US-11-060-756-197597	Sequence 197597,
C 32	13	72.2	25	10	US-11-060-756-197598	Sequence 197598,
C 33	12.8	71.1	17	6	US-10-459-876-17	Sequence 17, Appl
C 34	12.8	71.1	25	5	US-10-098-263B-37037	Sequence 37037, A
C 35	12.8	71.1	25	7	US-10-719-956-89806	Sequence 89806, A
36	12.8	71.1	25	7	US-10-719-956-558628	Sequence 558628,
37	12.8	71.1	25	8	US-10-719-900-28087	Sequence 28087, A
38	12.8	71.1	25	8	US-10-719-900-226025	Sequence 226025,
39	12.8	71.1	25	8	US-10-719-900-308249	Sequence 308249,
40	12.8	71.1	25	8	US-10-719-900-550905	Sequence 550905,
41	12.8	71.1	25	8	US-10-719-900-627829	Sequence 627829,
C 42	12.8	71.1	25	8	US-10-719-900-761202	Sequence 761202,
C 43	12.8	71.1	25	8	US-10-719-900-904924	Sequence 904924,
C 44	12.8	71.1	25	8	US-10-719-900-949533	Sequence 949533,
C 45	12.8	71.1	25	9	US-10-809-189-56205	Sequence 56205, A

ALIGNMENTS

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RESULT 1
US-10-659-948A-5
; Sequence 5, Application US/10659948A
; Publication No. US20040101946A1
; GENERAL INFORMATION:
; APPLICANT: Hovaneec, Timothy A
; TITLE OF INVENTION: Method of Using Ammonia-Oxidizing Bacteria
; FILE REFERENCE: 81289-294309
; CURRENT APPLICATION NUMBER: US/10/659,948A
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: US 09/573,684
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 60/386,217
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/386,218
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/386,219
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Oligonucleotide Probe
US-10-659-948A-5
Query Match 100.0%; Score 18; DB 7; Length 18;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCCCCCTTCTGATAC 18
Db 1 CCCCCCTTCTGATAC 18
RESULT 2
US-10-659-980A-5
; Sequence 5, Application US/10659980A
; Publication No. US20040106133A1
; GENERAL INFORMATION:
; APPLICANT: Hovaneec, Timothy A
; TITLE OF INVENTION: Method for Detecting Ammonia-Oxidizing Bacteria
; FILE REFERENCE: 81289-284781
; CURRENT APPLICATION NUMBER: US/10/659,980A
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; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: US 09/573,684
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 60/386,217
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/386,218
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/386,219
; PRIOR FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Oligonucleotide Probe
US-10-659-980a-5
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Query Match      100.0%; Score 18; DB 7; Length 18;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 CCCCCCTTCTTGATAC 18
        |||||
DB      1 CCCCCCTTCTTGATAC 18
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RESULT 3

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US-10-659-983a-5
; Sequence 5, Application US/10659983A
; Publication No. US20040157313A1
; GENERAL INFORMATION:
; APPLICANT: Hovaneq, Timothy A
; TITLE OF INVENTION: Ammonia-Oxidizing Bacteria
; FILE REFERENCE: 81289-284779
; CURRENT APPLICATION NUMBER: US/10/659,983A
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: US 09/573,684
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 60/386,217
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/386,218
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/386,219
; PRIOR FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Oligonucleotide Probe
US-10-659-983a-5
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Query Match      100.0%; Score 18; DB 7; Length 18;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 CCCCCCTTCTTGATAC 18
        |||||
DB      1 CCCCCCTTCTTGATAC 18
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RESULT 4

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US-10-719-956-558629
; Sequence 558629, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
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; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 558629
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-558629
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Best Local Similarity 93.8%; Pred. No. 2.4e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY      1 CCCCCCTTCTTGAT 16
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DB      4 CCCCCCTTCTTGAT 19
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RESULT 5

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US-09-320-337-74/c
; Sequence 74, Application US/09320337
; Patent No. US20010016352A1
; GENERAL INFORMATION:
; APPLICANT: Bohinski, Robert J.,
; APPLICANT: Whiteett, Jeffrey A.
; TITLE OF INVENTION: Nucleic Acid Sequences Controlling
; TITLE OF INVENTION: Lung Cell - Specific Gene Expression
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Carella, Byrne, Bain, Gilfillan, Cecchi, Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM P160
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: MS WORD 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/320,337
; FILING DATE: 26-MAY-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/442,809
; FILING DATE: 17-MAY-1995
; APPLICATION NUMBER: 08/245,356
; FILING DATE: 18-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Olstein, Elliot M.
; REGISTRATION NUMBER: 24,025
; REFERENCE/DOCKET NUMBER: 271010-447
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 973-994-1700
; TELEFAX: 973-994-1744
; INFORMATION FOR SEQ ID NO: 74:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: oligonucleotide
US-09-320-337-74
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Query Match      80.0%; Score 14.4; DB 3; Length 30;
Best Local Similarity 93.8%; Pred. No. 2.4e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
QY      2 CCCCCCTTCTTGAT 17
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Db 24 CCCCCCTTCTGGATGATA 9

RESULT 6

US-10-659-948A-21
; Sequence 21, Application US/10659948A
; Publication No. US20040101946A1
; GENERAL INFORMATION:
; APPLICANT: Hovanec, Timothy A
; TITLE OF INVENTION: Method of Using Ammonia-Oxidizing Bacteria
; FILE REFERENCE: 81289-294309
; CURRENT APPLICATION NUMBER: US/10/659,948A
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: US 09/573,684
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 60/386,217
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/386,218
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/386,219
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Oligonucleotide probe
US-10-659-948A-21

Query Match 76.7%; Score 13.8; DB 7; Length 18;
Best Local Similarity 88.2%; Pred. No. 4.9e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 CCCCCCTTCTGGATGAC 18
Db 2 CCCCCACTTCTGGACAC 18

RESULT 7

US-10-659-980A-21
; Sequence 21, Application US/10659980A
; Publication No. US20040106133A1
; GENERAL INFORMATION:
; APPLICANT: Hovanec, Timothy A
; TITLE OF INVENTION: Method for Detecting Ammonia-Oxidizing Bacteria
; FILE REFERENCE: 81289-284781
; CURRENT APPLICATION NUMBER: US/10/659,980A
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: US 09/573,684
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 60/386,217
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/386,218
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/386,219
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Oligonucleotide probe
US-10-659-980A-21

Query Match 76.7%; Score 13.8; DB 7; Length 18;
Best Local Similarity 88.2%; Pred. No. 4.9e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCCCCTTCTGGATGAC 18
Db 2 CCCCCACTTCTGGACAC 18

RESULT 8

US-10-659-983A-21
; Sequence 21, Application US/10659983A
; Publication No. US20040157313A1
; GENERAL INFORMATION:
; APPLICANT: Hovanec, Timothy A
; TITLE OF INVENTION: Ammonia-Oxidizing Bacteria
; FILE REFERENCE: 81289-284779
; CURRENT APPLICATION NUMBER: US/10/659,983A
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: US 09/573,684
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 60/386,217
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/386,218
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/386,219
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Oligonucleotide probe
US-10-659-983A-21

Query Match 76.7%; Score 13.8; DB 7; Length 18;
Best Local Similarity 88.2%; Pred. No. 4.9e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 CCCCCCTTCTGGATGAC 18
Db 2 CCCCCACTTCTGGACAC 18

RESULT 9

US-10-719-956-25535
; Sequence 25535, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 25535
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-25535

Query Match 76.7%; Score 13.8; DB 7; Length 25;
Best Local Similarity 88.2%; Pred. No. 4.8e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCCCTTCTGGATGATA 17
Db 3 CCGCCCTGTCTGGATA 19

RESULT 10

US-10-719-956-50560/c

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; Sequence 50560, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 50560
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-50560

Query Match
Best Local Similarity 76.7%; Score 13.8; DB 7; Length 25;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 CCCCCTCTTGATAC 18
DB 19 CCACCTCGCTGGATAC 3

RESULT 11
US-10-169-368-13/C
; Sequence 13, Application US/10169368
; Publication No. US20050070001A1
; GENERAL INFORMATION:
; APPLICANT: Kleelek, Knut
; APPLICANT: Brinkmann, Thomas
; APPLICANT: Goetting, Christian
; APPLICANT: Kuhn, Joachim
; TITLE OF INVENTION: Xylosyltransferase and isoforms thereof
; FILE REFERENCE: 020195-00002
; CURRENT APPLICATION NUMBER: US/10/169,368
; PRIOR FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: PCT/EP00/13311
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-10-169-368-13

Query Match
Best Local Similarity 76.7%; Score 13.8; DB 9; Length 28;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 CCCCCTCTTGATAC 18
DB 21 CCCCCTCTTGATAC 5

RESULT 12
US-10-719-956-94288
; Sequence 94288, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
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; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 94288
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-94288

Query Match
Best Local Similarity 74.4%; Score 13.4; DB 7; Length 25;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CCCCCTCTTGATGA 15
DB 4 CCCCCTCTTGATGA 18

RESULT 13
US-10-719-956-470164
; Sequence 470164, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 470164
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-470164

Query Match
Best Local Similarity 74.4%; Score 13.4; DB 7; Length 25;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 CCCCCTCTTGATGA 17
DB 11 CACCTCTTGATGA 25

RESULT 14
US-10-719-900-338352/C
; Sequence 338352, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 338352
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-338352

Query Match
Best Local Similarity 74.4%; Score 13.4; DB 8; Length 25;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 CCCCCTCTTGATAC 18
DB 22 CCCCCTCTTGATAC 8
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RESULT 15

US-10-719-900-416880
 ; Sequence 416880, Application US/10719900
 ; Publication No. US20050026164A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xue Mei Zhou
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
 ; FILE REFERENCE: 3528.1
 ; CURRENT APPLICATION NUMBER: US/10/719,900
 ; PRIOR FILING DATE: 2003-11-20
 ; PRIOR APPLICATION NUMBER: 60/427,808
 ; PRIOR FILING DATE: 2002.11.20
 ; NUMBER OF SEQ ID NOS: 982914
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO 416880
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 US-10-719-900-416880

Query Match 74.4%; Score 13.4; DB 8; Length 25;
 Best Local Similarity 93.3%; Pred. No. 7.7e+03;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 4 CCCTCTTCGATAC 18
 Db 4 CCCTCTTCGAGAC 18

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

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(without alignments)

505,921 Million cell updates/sec

Title: US-10-659-980A-5

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Total number of hits satisfying chosen parameters: 1026780

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Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 3: /cgn2_6/pdata/1/ina/6A COMB. seq:*
- 4: /cgn2_6/pdata/1/ina/6B COMB. seq:*
- 5: /cgn2_6/pdata/1/ina/H COMB. seq:*
- 6: /cgn2_6/pdata/1/ina/PC/US COMB. seq:*
- 7: /cgn2_6/pdata/1/ina/PC COMB. seq:*
- 8: /cgn2_6/pdata/1/ina/RE COMB. seq:*
- 9: /cgn2_6/pdata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	14.4	80.0	30	2	US-08-442-809A-74
C 2	13.4	74.4	15	3	US-09-396-196G-81113
C 3	12.8	71.1	17	3	US-09-583-610D-17
C 4	12.8	71.1	25	3	US-09-396-196G-56205
C 5	12.4	68.9	20	3	US-09-198-452A-2493
C 6	12.4	68.9	25	3	US-08-943-731-305
C 7	12.4	68.9	25	3	US-09-396-196G-24335
C 8	12.4	68.9	25	3	US-09-396-196G-45539
C 9	12.2	67.8	23	2	US-07-722-798A-77
C 10	12.2	67.8	25	3	US-09-396-196G-20092
C 11	12.2	67.8	25	3	US-09-396-196G-20103
C 12	12.2	67.8	27	2	US-08-480-473B-28
C 13	12.2	67.8	27	3	US-08-915-213-28
C 14	12.2	67.8	27	3	US-09-235-221-28
C 15	12.2	67.8	27	6	PCT-US96-10251-28
C 16	12	66.7	20	2	US-08-173-489C-17
C 17	12	66.7	20	3	US-10-002-623-451
C 18	11.8	65.6	18	3	US-09-289-377-10
C 19	11.8	65.6	20	3	US-09-495-714C-106
C 20	11.8	65.6	24	2	US-08-621-564B-3
C 21	11.8	65.6	24	3	US-09-269-220-3
C 22	11.8	65.6	25	3	US-09-538-709-290
C 23	11.8	65.6	25	3	US-09-396-196G-84823
C 24	11.6	64.4	23	2	US-07-722-798A-78

C 25	11.6	64.4	25	3	US-09-866-108A-11865	Sequence 11865, A
C 26	11.6	64.4	25	3	US-09-866-108A-11866	Sequence 11866, A
C 27	11.6	64.4	25	3	US-09-866-108A-11867	Sequence 11867, A
C 28	11.6	64.4	25	3	US-09-866-108A-11868	Sequence 11868, A
C 29	11.6	64.4	25	3	US-09-866-108A-11869	Sequence 11869, A
C 30	11.6	64.4	25	3	US-09-866-108A-11870	Sequence 11870, A
C 31	11.6	64.4	25	3	US-09-866-108A-11871	Sequence 11871, A
C 32	11.6	64.4	25	3	US-09-866-108A-11872	Sequence 11872, A
C 33	11.6	64.4	25	3	US-09-396-196G-10214	Sequence 10214, A
C 34	11.6	64.4	25	3	US-09-396-196G-103965	Sequence 103965,
C 35	11.6	64.4	25	3	US-09-396-196G-103966	Sequence 103966,
C 36	11.6	64.4	27	3	US-09-688-017-336	Sequence 336, App
C 37	11.6	64.4	30	2	US-08-479-817-1	Sequence 1, Appl1
C 38	11.6	64.4	30	2	US-08-461-038-1	Sequence 1, Appl1
C 39	11.6	64.4	30	2	US-08-461-645-1	Sequence 1, Appl1
C 40	11.6	64.4	30	3	US-08-221-543-1	Sequence 1, Appl1
C 41	11.6	64.4	30	3	US-09-451-905-42	Sequence 42, Appl1
C 42	11.4	63.3	17	3	US-08-584-040-5423	Sequence 5423, Ap
C 43	11.4	63.3	17	3	US-09-371-772B-2322	Sequence 2322, Ap
C 44	11.4	63.3	17	3	US-09-685-664B-2322	Sequence 2322, Ap
C 45	11.4	63.3	18	3	US-09-474-922A-14	Sequence 14, Appl1

ALIGNMENTS

RESULT 1
US-08-442-809A-74/c
; Sequence 74, Application US/08442809A
; Patent No. 5976873
; GENERAL INFORMATION:
; APPLICANT: Bohinski, Robert J.,
; APPLICANT: White, Jeffrey A.,
; TITLE OF INVENTION: Nucleic Acid Sequences
; TITLE OF INVENTION: Controlling Lung Cell -
; TITLE OF INVENTION: Specific Gene Expression
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Carella, Byrne, Baln, Gilfillan,
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/442, 809A
; FILING DATE: 17-MAY-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/245,356
; FILING DATE: 18-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Olstein, Elliot M.
; REGISTRATION NUMBER: 24,025
; REFERENCE/DOCKET NUMBER: 271010-360
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 74:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: oligonucleotide
; US-08-442-809A-74

Query Match 80.0%; Score 14.4; DB 2; Length 30;
Best Local Similarity 93.8%; Pred. No. 3.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCCCCCTCTCTGGATA 17
DB 24 CCCCCCTCTCTGGATA 9

RESULT 2
US-09-396-196G-81113/C
; Sequence 81113, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 81113
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-81113

Query Match 74.4%; Score 13.4; DB 3; Length 25;
Best Local Similarity 93.3%; Pred. No. 1.1e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CCCCCCTCTCTGGATA 17
DB 23 CCCCCCTCTCTGGATA 9

RESULT 3
US-09-583-610D-17
; Sequence 17, Application US/09583610D
; Patent No. 6740735
; GENERAL INFORMATION:
; APPLICANT: Glanville, S.H.
; APPLICANT: Bradley, W.A.
; TITLE OF INVENTION: DNA Encoding Human apob48r: A Monocyte-Macrophage
; TITLE OF INVENTION: Apolipoprotein B48 Receptor Gene and Protein
; FILE REFERENCE: D5880CIP
; CURRENT APPLICATION NUMBER: US/09/583,610D
; CURRENT FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: US 09/130,242
; PRIOR FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 22
; SEQ ID NO 17
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense primers were based on the 5'-end
; OTHER INFORMATION: sequence of the THP-1 (73 clone (bp 2203-2187
US-09-583-610D-17

Query Match 71.1%; Score 12.8; DB 3; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.1e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCCCCCTCTCTGGAT 16
DB 1 CCAGCCTCTCTGGAT 16

RESULT 4
US-09-396-196G-56205/C
; Sequence 56205, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56205
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-56205

Query Match 71.1%; Score 12.8; DB 3; Length 25;
Best Local Similarity 87.5%; Pred. No. 2.3e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCCCCCTCTCTGGATA 17
DB 23 CCAGCCTCTCTGGAGA 8

RESULT 5
US-09-198-452A-2493
; Sequence 2493, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffith, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prev
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 2493
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-2493

Query Match 68.9%; Score 12.4; DB 3; Length 20;
Best Local Similarity 92.9%; Pred. No. 3.5e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CCTCTCTCTGGATAC 18
DB 4 CCTCTCTCTGGATTC 17

RESULT 6
US-08-943-731-305/C
; Sequence 305, Application US/08943731
; Patent No. 6265157
; GENERAL INFORMATION:
; APPLICANT: PROCKOP, DARWIN J.
; APPLICANT: SPOTILA, LORETTA D.
; APPLICANT: DELTAS, CONSTANTINOS D.
; APPLICANT: SEREDA, LARISA
; APPLICANT: LARSON, ANDREA W.
; APPLICANT: PACK, MICHAEL

APPLICANT: COLLIGE, ALAIN
APPLICANT: EARLY, JAMES
APPLICANT: KORKIO, JARMO
APPLICANT: ALA-KOKKO, LENA, et al.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING
TITLE OF INVENTION: ALTERED TYPE I OR TYPE IX COLLAGEN GENE SEQUENCES
NUMBER OF SEQUENCES: 666
CORRESPONDENCE ADDRESS:
ADDRESSER: PANTICH SCHWARZE JACOBS & NADEL, P.C.
STREET: ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND
STREET: FLR.
CITY: PHILADELPHIA
STATE: PA
COUNTRY: USA
ZIP: 19103-7086
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,731
FILING DATE: 03-OCT-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,322
FILING DATE: 14-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/803,628
FILING DATE: 03-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: DOYLE LEARY Ph.D., KATHRYN
REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET INFORMATION: 9598-27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-965-1284
TELEFAX: 215-567-2991
TELEX: 8311494
INFORMATION FOR SEQ ID NO: 305:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-943-731-305

Query Match 68.9%; Score 12.4; DB 3; Length 25;
Best Local Similarity 92.9%; Pred. No. 3.6e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CCCCTCTCTGGAT 16
DB 24 CCCCTCTCTGGAT 11

RESULT 7
US-09-396-196G-24325
Sequence 24325, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Miltmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 24325
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-09-396-196G-24325

Query Match 68.9%; Score 12.4; DB 3; Length 25;
Best Local Similarity 92.9%; Pred. No. 3.6e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CCCCTCTCTGGATA 17
DB 3 CCCCTCTCTGGAGA 16

RESULT 8
US-09-396-196G-45539
Sequence 45539, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Miltmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 45539
LENGTH: 25
TYPE: DNA
ORGANISM: mus musculus
US-09-396-196G-45539

Query Match 68.9%; Score 12.4; DB 3; Length 25;
Best Local Similarity 92.9%; Pred. No. 3.6e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CCCCTCTCTGGATA 17
DB 1 CCCACTCTCTGGATA 14

RESULT 9
US-07-722-798A-77
Sequence 77, Application US/07722798A
Patent No. 5427930
GENERAL INFORMATION:
APPLICANT: Larry G. Birkenmeyer
APPLICANT: John J. Carrino
APPLICANT: Bruce J. Dille
APPLICANT: Hsiang-Yun Hu
APPLICANT: Jon David Kratochvil
APPLICANT: Thomas G. Laffier
APPLICANT: Ronald L. Marshall
APPLICANT: Laurie A. Rinhardt
APPLICANT: Natalie A. Solomon
TITLE OF INVENTION: AMPLIFICATION OF TARGET NUCLEIC
NUMBER OF INVENTION: ACIDS USING GAP FILLING LIGASE CHAIN REACTION
NUMBER OF SEQUENCES: 124
CORRESPONDENCE ADDRESS:
ADDRESSER: Abbott Laboratories
STREET: One Abbott Park Road
CITY: Abbott Park
STATE: Illinois
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy diskette

```

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Nordperfect 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/722.798A
; FILING DATE: 19910628
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas D. Bralnard
; REGISTRATION NUMBER: 32,459
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-4884
; TELEFAX: 708-937-9556
; INFORMATION FOR SEQ ID NO: 77:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid (synthetic DNA)
US-07-722-798A-77

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```

Query Match 67.8%; Score 12.2; DB 2; Length 23;
Best Local Similarity 82.4%; Pred. No. 4.6e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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```

Qy 2 CCCCTCTTCTGGATAC 18
Db 1 CCCCTGTCTGTTCC 17

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RESULT 10
US-09-396-196G-20092/c
; Sequence 20092, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20092
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-20092

```

```

Query Match 67.8%; Score 12.2; DB 3; Length 25;
Best Local Similarity 82.4%; Pred. No. 4.6e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

Qy 2 CCCCTCTTCTGGATAC 18
Db 20 CCACCTCGCTGGATAC 4

```

```

RESULT 11
US-09-396-196G-20103/c
; Sequence 20103, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.

```

```

; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20103
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-20103

```

```

Query Match 67.8%; Score 12.2; DB 3; Length 25;
Best Local Similarity 82.4%; Pred. No. 4.6e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

Qy 2 CCCCTCTTCTGGATAC 18
Db 18 CCACCTCGCTGGATAC 2

```

```

RESULT 12
US-08-480-473B-28/c
; Sequence 28, Application US/08480473B
; Patent No. 5882914
; GENERAL INFORMATION:
; APPLICANT: Semenza, Gregg L.
; TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,473B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/053001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-480-473B-28

```

```

Query Match 67.8%; Score 12.2; DB 2; Length 27;
Best Local Similarity 82.4%; Pred. No. 4.7e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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```

Qy 1 CCCCTCTTCTGGATTA 17
Db 27 CCCCTTTTCAAGATA 11

```

RESULT 13

Mon Apr 10 08:45:42 2006

US-08-915-213-28/c
Sequence 28, Application US/08915213
Patent No. 6020462
GENERAL INFORMATION:
APPLICANT: Semenza, Gregg L.
TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,213
FILING DATE: 20-AUG-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/480,473
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/053001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-915-213-28

Query Match 67.8%; Score 12.2; DB 3; Length 27;
Best Local Similarity 82.4%; Pred. No. 4.7e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCCCCTTCTGATA 17
DB 27 CCCCCCTTTCAGATA 11

RESULT 14
US-09-235-217-28/c
Sequence 28, Application US/09235217
Patent No. 6222018
GENERAL INFORMATION:
APPLICANT: Semenza, Gregg L.
TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/235,217

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/480,473
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/053001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-235-217-28

Query Match 67.8%; Score 12.2; DB 3; Length 27;
Best Local Similarity 82.4%; Pred. No. 4.7e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCCCCTTCTGATA 17
DB 27 CCCCCCTTTCAGATA 11

RESULT 15
PCT-US96-10251-28/c
Sequence 28, Application PC/TUS9610251
GENERAL INFORMATION:
APPLICANT: The Johns Hopkins University School of Medicine
TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10251
FILING DATE: 06-JUN-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/053001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
PCT-US96-10251-28

Query Match 67.8%; Score 12.2; DB 6; Length 27;
Best Local Similarity 82.4%; Pred. No. 4.7e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 CCCCCCTTCTGGATA 17
||| ||| ||| |||
Db 27 CCCCCCTTCTGGATA 11

Search completed: April 7, 2006, 08:41:14
Job time : 64.2432 secs

18.

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using bw model

Run on: April 7, 2006, 08:38:51 ; Search time 2905.78 Seconds
(without alignments)
289.825 Million cell updates/sec

Title: US-10-659-980A-5
Perfect score: 18
Sequence: 1 ccccccctctcgcgatac 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 52094

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*
10: gb_est10:*
11: gb_est11:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	12.2	67.8	26	11	TA25G06P
2	11.8	65.6	22	9	AZ817329
3	11.8	65.6	28	8	AZ817329
4	11.8	65.6	28	8	AZ817329
5	11.8	65.6	28	8	AZ817329
6	11.6	64.4	23	9	AZ817329
7	11.4	63.3	13	5	BQ589768
8	11.4	63.3	26	9	BQ589768
9	11.2	62.2	22	1	A1039313
10	11.1	61.1	19	9	AZ817329
11	11.1	61.1	20	9	AZ817329
12	11.1	61.1	25	9	AZ817329
13	11.1	61.1	26	8	D18736
14	10.8	60.0	23	9	AZ817329
15	10.8	60.0	25	1	A1915575
16	10.8	60.0	28	1	A1649190
17	10.8	60.0	29	8	CR001953
18	10.8	60.0	30	9	AZ817329
19	10.6	58.9	23	9	AZ817329
20	10.6	58.9	23	9	AZ817329
21	10.6	58.9	25	8	CR001953
22	10.6	58.9	26	9	AZ817329

c	23	10.6	58.9	28	9	AZ647874	AZ647874	1M0514D07
c	24	10.6	58.9	30	1	AU251318	AU251318	AU251318
c	25	10.6	58.9	30	10	C2472794	C2472794	d02410-5P
c	26	10.4	57.8	17	10	AJ599163	AJ599163	Arabidops
c	27	10.4	57.8	22	8	DR026424	DR026424	Osmo00431
c	28	10.4	57.8	22	8	AZ826662	AZ826662	2M0253J05
c	29	10.4	57.8	24	9	AZ404465	AZ404465	1M0172P09
c	30	10.4	57.8	24	11	TA185C06P	TA185C06P	TA185C06P
c	31	10.4	57.8	25	1	A1628239	A1628239	cy3C04.x
c	32	10.4	57.8	26	1	AU265518	AU265518	AU265518
c	33	10.4	57.8	27	9	AZ776617	AZ776617	2M0010D23
c	34	10.4	57.8	28	9	BH030856	BH030856	SAK_1035
c	35	10.4	57.8	29	5	BQ590098	BQ590098	BR12643-0
c	36	10.4	57.8	29	9	AZ307991	AZ307991	1M0010F01
c	37	10.4	57.8	30	5	BQ590438	BQ590438	BR12643-0
c	38	10.4	57.8	30	9	AZ804486	AZ804486	2M0065D07
c	39	10.2	56.7	22	1	AA996014	AA996014	0826D08.s
c	40	10.2	56.7	25	1	AA894827	AA894827	0161008.s
c	41	10.2	56.7	25	11	TA115D09Q	TA115D09Q	TA115D09Q
c	42	10.2	56.7	26	10	AG203573	AG203573	AG203573
c	43	10.2	56.7	28	1	AA905471	AA905471	OK0111.8
c	44	10.2	56.7	28	9	AZ853408	AZ853408	2M0156P01
c	45	10.2	56.7	28	10	CL663977	CL663977	PR101454

ALIGNMENTS

RESULT 1	TA25G06P/c	26 bp	DNA	linear	GSS	13-DEC-2000
LOCUS	TA25G06P	26 bp	DNA	linear	GSS	13-DEC-2000
DEFINITION	T. brucei sheared genomic DNA clone 25g06, forward sequence,					
ACCESSION	AL453426					
VERSION	AL453426.1	GI:11849213				
KEYWORDS	Genomic survey sequence.					
SOURCE	Trypanosoma brucei					
ORGANISM	Trypanosoma brucei					
REFERENCE	1 (bases 1 to 26)					
AUTHORS	Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrett, B.G.					
TITLE	Direct Submission					
JOURNAL	Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrett@sanger.ac.uk and nh@sanger.ac.uk					
COMMENT	Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrett, Oxford University Press, 1999).					
FEATURES	Source					
ORIGIN	1..26					
	/organism="Trypanosoma brucei"					
	/mol_type="genomic DNA"					
	/strain="TREU927"					
	/db_xref="taxon:5691"					
	/clone="25g06"					
Query Match	67.8%	Score 12.2	DB 11	Length 26		
Best Local Similarity	82.4%	Pred. No. 2.5e+05				
Matches	14	Conservative	0	Mismatches	3	Indels
				Gaps	0	

```

Qy      1  CCCCCCTCTTCTGATA 17
          |||||
Db      25  CCCCCCTCTTCATGAA  9

```

LOCUS	AZ817329	22 bp	DNA	linear	GSS 20-FEB-2001
DEFINITION	2M086D22R Mouse 10kb plasmid UUGC1M library Mus musculus genomic				
	clone UUGC2M086D22 R, genomic survey sequence.				

ACCESSION	AZ817329
VERSION	AZ817329.1
	GI:12987333

SOURCE Mus musculus (house mouse)

ORGANISM

REFERENCE
AUTHORS
1 (bases 1 to 22)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

TITLE Mouse whole genome scaffolding with paired end reads from 10Kb

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss

Rm. 308, Biometrical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel.: 801 585 5606
Fax: 801 585 7177
Email: gdm@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0086 row: D column: 22
Seq primer: CACACAGAAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.

FEATURES	Location/Qualifiers
source	1. .22

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/organism="Mus musculus"  
/mol_type="genomic DNA"  
/strain="C57BL/6J"  
/db_xref="taxon:10090"  
/clone="UUGC2M0086D2"
```

lab host: E. coli strain XL10-Gold, T1-resistant, F⁻ /clone: lib="Mouse 10kb plasmid UGCGM library"
note="Vector: pMD24env, Purified genomic DNA from M. musculus C57BL/6j (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repeated with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The ligated DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD24 (gil1473111[gb]AP129072.1), a copy-number of pMD24 derivative of plasmid R1'. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to purified vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match	65.6%;	Score 11.8;	DB 9;	Length 22
Best Local Similarity	86.7%;	Pred. No. 3.8e+05;		

	Matches	13; Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;
Qy	1	CCCCCCTTGTGA	15						
Db	8	CCCCCTTTCTGAA	22						

[illegible]

IMAGE:134310 3 BLAST hit to
PROTEIN - ; mRNA sequence.
B54679

ACCESSION	R54679
VERSION	R54679.1
	GI:819137

SOURCE	Homo sapiens (human)
1. <i>Chimpanzee</i>	98.6%
2. <i>Orangutan</i>	96.8%
3. <i>Gorilla</i>	95.8%
4. <i>Macaque</i>	93.2%
5. <i>Mouse</i>	85.0%
6. <i>Rat</i>	82.0%
7. <i>Chicken</i>	75.0%
8. <i>Fruit fly</i>	60.0%
9. <i>Yeast</i>	50.0%
10. <i>Plant</i>	40.0%

ORGANISM

REFERENCE

AUTHORS

1 (bases 1 to 28)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., ...
Hawkins, M., Hillier, L., Jones, C.

Parsons, J., Kilkin, L., Konling, I., Soares, M., Lau, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
Wilson, R.

TITLE	JOURNAL	COMMENT
The WashU-Merck EST Project	Unpublished (1995)	Contact: Wilson RK

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel.: 314 266 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

```

Insert Size: 718
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LULU This clone is available royalty-free
through LULU; contact the IMAGE Consortium (info@image.llnl.gov)
for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Insert Length: 718 Std Error: 0.00

```

Seq primer: M13Rpr1
High quality sequence stop: 1.

```

FEATURES
source      Location/Qualifiers
1. . 28    /usr/include/asm/hwmon.h

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:566948"
/db_xref="taxon:9606"
/clone="IMAGE:154510"
/sex="Female"
/dev_stage="adult"
/lab_host="MDH108 (ampicillin resistant)"
/clone_lib="Scars Breast 2NHBac"
/notes="Organ: breast; Vector: pUT3D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer (5'
TGTTGCAATCTGTGAAGGCGAGCGCGCTTTTCTTTTCTTTT 3').
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of a modified pUT3 vector (Pharmacia).
Library went through one round of normalization to a Cot
230. Library constructed by Bento Soares and M.Patima
Bonaldo."

```

ORIGIN

Query Match	65.6%	Score 11.8	DB 8	Length 28
Best Local Similarity	86.7%	Pred. No. 3.9e+05		
Matches 13; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0

2 CCCCCTCTCTGGAT 16

Db 25 CGCCCTCTCTGAT 11

RESULT 4
A2489682/c 28 bp DNA 1linear GSS 05-OCT-2000
LOCUS 1M032G16P Mouse 10kb plasmid UGCI1M library Mus musculus genomic
DEFINITION clone UGCI1M032G16 P, genomic survey sequence.
ACCESSION A2489682
VERSION A2489682.1 GI:10659670
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 28)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0322 row: G column: 16
Seq primer: CGTTGTAAACGACGCCACGT
Class: plasmid ends
High quality sequence stop: 28.
Location/Qualifiers
1..28
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCI1M032G16"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UGCI1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (GI:4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 65.6%; Score 11.8; DB 9; Length 28;
Best Local Similarity 86.7%; Pred. No. 3.9e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OR 1 CCCCTCTCTGGA 15

Db 18 CCCCTCTCTGGA 4

RESULT 5
C2443094 28 bp DNA 1linear GSS 07-APR-2005
LOCUS 1BB8D03.fwd HIV-vector integration sites from well-expressed
DEFINITION proviruses in human Jurkat T cells Homo sapiens genomic clone
ACCESSION C2443094
VERSION C2443094.fwd, genomic survey sequence.
KEYWORDS C2443094.1 GI:62379366
GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 28)
Lewinski,M.K., Blasgrove,D., Shinn,P., Chen,H., Hoffmann,C., Hammenhall,S., Verdin,E., Berry,C.C., Ecker,J.R. and Bushman,F.D.
Genome-wide analysis of chromosomal features repressing human immunodeficiency virus transcription
J. Virol. 79 (11), 6610-6619 (2005)
15890899
Contact: Bushman FD
Department of Microbiology
University of Pennsylvania School of Medicine
402C Johnson Pavilion, 3610 Hamilton Walk, Philadelphia, PA 19104-6076, USA
Tel: 215 573 8732
Fax: 215 573 4856
Email: bushman@mail.med.upenn.edu
Class: PCR with specific primers.
Location/Qualifiers
1..28
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="1BB8D03.fwd"
/cell_line="Jurkat"
/clone_1lb="HIV-vector integration sites from well-expressed proviruses in human Jurkat T cells"
/note="Vector: LTR-Tat-IREs-GFP (pBV711); We have investigated regulatory sequences in noncoding human DNA that are associated with repression of an integrated human immunodeficiency virus type 1 (HIV-1) promoter. HIV-1 integration results in the formation of precise and homogeneous junctions between viral and host DNA, but integration takes place at many locations. Thus, the variation in HIV-1 gene expression at different integration sites reports the activity of regulatory sequences at nearby chromosomal positions. Negative regulation of HIV transcription is of particular interest because of its association with maintaining HIV in a latent state in cells from infected patients. To identify chromosomal regulators of HIV transcription, we infected Jurkat T cells with an HIV-based vector transducing green fluorescent protein (GFP) and separated cells into populations containing well-expressed (GFP-positive) or poorly expressed (GFP-negative) proviruses. We then determined the chromosomal locations of the two classes by sequencing 971 junctions between viral and cellular DNA. Possible effects of endogenous cellular transcription were characterized by transcriptional profiling. Low-level GFP expression correlated with integration in (i) gene deserts, (ii) centromeric heterochromatin, and (iii) very highly expressed cellular genes. These data provide a genome-wide picture of chromosomal features that repress transcription and suggest models for transcriptional latency in cells from HIV-infected patients."

ORIGIN

OR 1 CCCCTCTCTGGA 15

Query Match 65.6%; Score 11.8; DB 10; Length 28;
 Beet Local Similarity 86.7%; Pred. No. 3.9e+05;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 CCCCTCTCTGATGATA 17
 |||||
 DB 14 CCCCTCTCTGATGATA 28

RESULT 6
 A2785027/c 23 bp DNA linear GSS 16-FEB-2001

LOCUS A2785027 Mouse 10kb plasmid UUGCM library Mus musculus genomic
 DEFINITION cDNA UUGCM0028H03 R, genomic survey sequence.

ACCESSION A2785027 GI:12921357

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 23)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weis, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weis
 University of Utah
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: bdunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
 Plate: 0028 row: H column: 03
 Seq primer: CACACAGGAAACGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 23.

FEATURES
 source Location/Qualifiers

1..23
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGCM0028H03"
 /sex="Male"
 /lab_host="R. Colt strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGCM library"
 /note="Vector: pMD22v; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (GI:4732114|db|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN

Query Match 64.4%; Score 11.6; DB 9; Length 23;
 Beet Local Similarity 77.8%; Pred. No. 4.8e+05;
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCCCCCTCTCTGATGATAC 18
 |||||
 DB 20 CCCCCCTCTCTGATGATAC 3

RESULT 7

B0589768

LOCUS B0589768 13 bp mRNA linear EST 06-DEC-2002
 DEFINITION B012680-024-020-D03-SP6 MP12-ADIS-024-storage root Beta vulgaris
 cDNA clone 024-020-D03 5-PRIME, mRNA sequence.

ACCESSION B0589768

VERSION B0589768.1 GI:26119351

KEYWORDS EST.

SOURCE Beta vulgaris

ORGANISM Beta vulgaris

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Eudicotyledons; Magnoliophyta; eudicotyledons; core eudicotyledons;
 Caryophyllales; Amaranthaceae; Beta.
 1 (bases 1 to 13)
 Herwig, R., Schulz, B., Weishaar, B., Hennig, S., Steinfath, M.,
 Drungowski, M., Stahl, D., Wuck, W., Menze, A., O'Brien, J., Lennrich, H.
 and Radloff, U.

TITLE Construction of a 'unigenes' cDNA clone set by oligonucleotide
 fingerprinting allows access to 25 000 potential sugar beet genes
 JOURNAL Plant J. 32 (5), 845-857 (2002)
 COMMENT Contact: Weishaar B
 ADIS DNA core facility at MP12
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weisshaar@mplz-koeln.mpg.de

Insert Length: 13 Std Error: 0.00
 Plate: 20 row: D column: 03
 Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
 Location/Qualifiers

FEATURES
 source Location/Qualifiers

1..13
 /organism="Beta vulgaris"
 /mol_type="mRNA"
 /cultiivar="KWS2320 (double haploid, monogerm breeding
 line)"
 /db_xref="GABI:190356"
 /db_xref="taxon:161934"
 /clone="024-020-D03"
 /tissue_type="storage root"
 /lab_host="EMD110B"
 /clone_lib="MP12-ADIS-024-storage root"
 /note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
 cDNA library from sugar beet, library provided by KWS
 Kleinfeldener Saatgut AG Einbeck, Germany, contact:
 b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
 orientation:
 SP6-SalI-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
 Sequencing granted in the context of the GABI-Beet
 project, local PI: Dr. Katharina Schneider, coordinator:
 Prof. Christian Jung; Sequence submission managed by
 RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN

Query Match 63.3%; Score 11.4; DB 5; Length 13;
 Beet Local Similarity 92.3%; Pred. No. 5.7e+05;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CCCCTCTCTGAT 16
 |||||
 DB 1 CCCCTCTCTGAT 13

ORIGIN

RESULT 8
AZ487733
LOCUS
DEFINITION 26 bp DNA linear GSS 05-OCT-2000
1M0317A10R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0317A10 R, genomic survey sequence.
ACCESSION
AZ487733
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 26)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0317 row: A column: 10
Seq primer: CACACAGGAAACAGCATATACC
Class: Plasmid ends
High quality sequence stop: 26.
Location/Qualifiers
1..26
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCIM0317A10"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42nv, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (g14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 63.3%; Score 11.4; DB 9; Length 26;
Best Local Similarity 92.3%; Pred. No. 6.1e+05;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 4 CCGCTTCTGGAT 16
|||||||
Db 10 CCGCTTCTGGAT 22

RESULT 9
A1039313
LOCUS
DEFINITION 22 bp mRNA linear EST 24-SEP-1998
ox36b04.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone
IMAGE:1658383 3' similar to SW-TP33_HUMAN p49746 THROMBOSPONDIN 3
PRECURSOR, contains Alu repetitive element, mRNA sequence.
ACCESSION
A1039313
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 22)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapsb-remail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Insert length: 954 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amer sham
High quality sequence stop: 1.
Location/Qualifiers
1..22
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1658383"
/dev_stage="8-9 weeks"
/lab_host="DH10B"
/note="Cloned from total_fetus_Nb2HF8_9w"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from pooled 8-9 week
(total) fetus material with a Not I - oligo(dT) primer [5'
TGTTACCACTGGAAGTGGAGCGCCCTTAATTCTTTTCTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptor
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN
Query Match 62.2%; Score 11.2; DB 1; Length 22;
Best Local Similarity 81.2%; Pred. No. 7.6e+05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 1 CCGCCCTCTGGAT 16
|||||||
Db 5 CCGCCCTCTGGAT 20

RESULT 10
AZ875769
LOCUS
DEFINITION 19 bp DNA linear GSS 21-FEB-2001
2M0190A02R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC2M0190A02 R, genomic survey sequence.
ACCESSION
AZ875769
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,

TITLE
 Reilly,M., Rose,M., Wright,R., Stokes,R., Tingey,A., von
 Niederhausen,A. and Wright,D.,Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL
 COMMENT
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0190 row: A column: 02
 Seg primer: CACACGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 19.

FEATURES

source

1..19
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUCGCM0190A02"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUCGCM library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 (g14732114[gblAP129072.1], a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN

Query Match 61.1%; Score 11; DB 9; Length 19;
 Best Local Similarity 100.0%; Pred. No. 9.4e+05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCTCTTCTGGA 15
 |||||
 Db 1 CCTCTTCTGGA 11

RESULT 11
 AZ627859 20 bp DNA linear GSS 13-DEC-2000
 LOCUS 1M0476B04F Mouse 10kb plasmid UUCGCM library Mus musculus genomic
 DEFINITION clone UUCGCM0476B04 F, genomic survey sequence.
 ACCESSION AZ627859
 VERSION AZ627859.1 GI:11750145
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 20)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

TITLE
 Irlam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausen,A. and Wright,D.,Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL
 COMMENT
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0476 row: E column: 04
 Seg primer: CGTTGTAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 20.

FEATURES

source

1..20
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUCGCM0476B04"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUCGCM library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 (g14732114[gblAP129072.1], a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN

Query Match 61.1%; Score 11; DB 9; Length 20;
 Best Local Similarity 100.0%; Pred. No. 9.4e+05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCTCTTCTGG 14
 |||||
 Db 3 CCTCTTCTGG 13

RESULT 12
 AZ585557 25 bp DNA linear GSS 13-DEC-2000
 LOCUS 1M0390M18R Mouse 10kb plasmid UUCGCM library Mus musculus genomic
 DEFINITION clone UUCGCM0390M18 R, genomic survey sequence.
 ACCESSION AZ585557
 VERSION AZ585557.1 GI:11707559
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 25)

AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

JOURNAL
COMMENT
Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0390 row: M column: 18
Seq primer: CACACAGCAACACGCTATGACC
Class: plasmid ends
High quality sequence stop: 25.

FEATURES
source
1..25
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCGM0390M18"
/sex="Male"
/lab_host="B. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCGM library"
/note="Vector: PMD29v; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent B. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 61.1%; Score 11; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 9.7e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 4 CCCCTCTCTGG 14
|||||
20 CCCCTCTCTGG 10

Db 20 CCCCTCTCTGG 10

RESULT 13
D18736 26 bp mRNA linear EST 09-FEB-2005
LOCUS D18736
DEFINITION MUSGS01798 Mouse 3'-directed Mus musculus cDNA clone md0836 3',
mRNA sequence.
ACCESSION D18736
VERSION D18736.1 GI:1100705
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
1 (bases 1 to 26)
AUTHORS
Kawamoto,S., Okubo,K., Yoshii,J., Katsuki,M. and Matsubara,K.
TITLE
Analysis of gene expression in mouse embryogenesis by 3'-directed
cDNA sequencing
Unpublished (1995)

JOURNAL
COMMENT
Contact: Shoko Kawamoto
Institute for Cellular and Molecular Biology
Osaka University
1-3, Yamadaoka, Suita, Osaka, 565, Japan
Email: shoko@next.imb.osaka-u.ac.jp.

FEATURES
source
1..26
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="md0836"
/tissue_type="decidual tissue (day 6.5-8.5 of gestation)"
/clone_lib="Mouse 3'-directed"

ORIGIN
Query Match 61.1%; Score 11; DB 8; Length 26;
Best Local Similarity 100.0%; Pred. No. 9.7e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 6 CTCTTCTGGAT 16
|||||
12 CTCTTCTGGAT 2

Db 12 CTCTTCTGGAT 2

RESULT 14
AZ592213 23 bp DNA linear GSS 13-DEC-2000
LOCUS D18736
DEFINITION IM040223R Mouse 10kb plasmid UUCGM library Mus musculus genomic
clone UUCGM040223 R, genomic survey sequence.
ACCESSION AZ592213
VERSION AZ592213.1 GI:11714403
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 23)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

JOURNAL
COMMENT
Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0402 row: P column: 23
Seq primer: CACACAGCAACACGCTATGACC
Class: plasmid ends
High quality sequence stop: 23.

FEATURES
source
1..23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCGM040223R"
/sex="Male"
/lab_host="B. Coli strain XL10-Gold, T1-resistant, F-"

/clone_11b="Mouse 10kb plasmid UUC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (g1|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 60.0%; Score 10.8; DB 9; Length 23;
Best Local Similarity 85.7%; Pred. No. 1.2e+06;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CCTCTTCTGGATAC 18
|||||
DB 3 CCTCTTCTGGACAC 16

RESULT 15
AI915575/c 25 bp mRNA 1linear EST 28-JUL-1999

LOCUS tr40909.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2220832 3'
DEFINITION similar to SW:PI00 HUMAN P30808 DNA-BINDING P52/PI00 COMPLEX, 100
KD SUBUNIT; contains element MSRI repetitive element;; mRNA
sequence.

ACCESSION AI915575 GI:5635430
VERSION AI915575.1
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.

REFERENCE 1 (bases 1 to 25)
AUTHORS NCI_CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strauberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution Information can be
found through the I.M.A.G.E. Consortium/LNL at:
www.bio.lnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers

FEATURES
source 1..25
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2220832"
/tissue_type="tumor, 5 pooled (see description)"
/lab_host="DH10B"

/clone_11b="NCI_CGAP_Ov23"
/note="Organ: ovary; Vector: pCMV-Sport6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.35 kb. Tumor types include: mixed
Mullerian tumor, papillary serous, clear cell, spindle
cell. All are primary tumors, metastasis positive. Life
Technologies catalog #: 11534-013"

ORIGIN

Query Match 60.0%; Score 10.8; DB 1; Length 25;
Best Local Similarity 85.7%; Pred. No. 1.2e+06;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCCCCCTTCTGG 14
|||||
DB 19 CCCCCCTTCTTGG 6

Search completed: April 7, 2006, 10:30:59
Job time : 2907.78 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 7, 2006, 08:38:45; Search time 357.081 Seconds
(without alignments)
335.959 Million cell updates/sec

Title: US-10-659-980A-5
Perfect score: 18
Sequence: 1 cccccctctcgtgac 18

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 4936997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 4138570

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: N GeneSeq 21:*

- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001s:*
- 5: geneseqn2002s:*
- 6: geneseqn2003s:*
- 7: geneseqn2004s:*
- 8: geneseqn2005s:*
- 9: geneseqn2006s:*
- 10: geneseqn2007s:*
- 11: geneseqn2008s:*
- 12: geneseqn2009s:*
- 13: geneseqn2010s:*
- 14: geneseqn2011s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	6	ABA02420
2	18	100.0	18	12	ABA02420
3	14.4	80.0	30	4	AA01828
4	13.8	76.7	18	12	ADW32724
5	13.4	74.4	22	12	ADL32573
6	13.2	73.3	20	10	ADG36420
7	13.2	73.3	27	12	ADG31445
8	13.2	73.3	27	12	ADK41856
9	13.2	73.3	28	10	ADG36414
10	13.2	73.3	30	8	ACA54549
11	13.2	73.3	30	8	ABX13526
12	12.8	71.1	17	10	ADH30251
13	12.8	71.1	17	12	ADG00840
14	12.8	71.1	18	12	ADN08161
15	12.8	71.1	25	9	ACT137046
16	12.6	70.0	24	14	ADZ08754
17	12.4	68.9	17	3	AA02030
18	12.4	68.9	17	3	AA02029

20	12.4	68.9	20	2	AA031192
C	21	12.4	20	6	ABX03745
C	22	12.4	20	13	ABX13323
C	23	12.4	20	12	ADN02302
C	24	12.4	20	13	ADR68924
C	25	12.4	25	5	AA022073
C	26	12.4	25	5	AA022073
C	27	12.4	25	2	AA019119
C	28	12.2	17	2	AA017514
C	29	12.2	17	8	ABX65019
C	30	12.2	17	14	ADZ34093
C	31	12.2	18	3	AA014813
C	32	12.2	19	10	ADP36053
C	33	12.2	19	10	ADP36480
C	34	12.2	19	11	ADL79197
C	35	12.2	19	11	ADL78948
C	36	12.2	19	12	ADQ14296
C	37	12.2	19	14	ADY87306
C	38	12.2	19	14	ADY87733
C	39	12.2	20	14	ADZ84877
C	40	12.2	20	14	ADZ84729
C	41	12.2	21	13	ADU42656
C	42	12.2	23	2	AA036081
C	43	12.2	23	2	AA039338
C	44	12.2	23	6	ABX24426
C	45	12.2	24	10	ADZ40344
				14	ADW38589

ALIGNMENTS

RESULT 1	ABA02420	standard; DNA; 18 BP.
ID	ABA02420	
XX	ABA02420;	
AC	29-AUG-2003 (revised)	
XX	DT 04-MAR-2002 (first entry)	
XX		
XX	Type A/A1 ammonia-oxidising bacterium 16S rRNA gene probe.	
DE		
XX		
XX	Type A, type A1, ammonia-oxidising bacterium; AOB, nitrite;	
KM	16S rRNA gene; ribosomal RNA; aquaria; aquaculture;	
KM	waste water treatment; bioremediation; probe; ss.	
XX		
OS	Nitrosomonadales.	
XX		
PM	WO200190312-A1.	
XX		
PD	29-NOV-2001.	
XX		
PF	17-MAY-2001; 2001WO-US016265.	
XX		
PR	19-MAY-2000; 2000US-00573684.	
XX		
PA	(AQUA-) AQUARIA INC.	
XX		
PI	Hovane TA, Burrell PC,	
XX		
DR	WPI; 2002-075367/10.	
XX		
PT	New bacteria capable of oxidizing ammonia to nitrite, for preventing or	
PT	alleviating the accumulation of ammonia in fresh water aquaria, seawater	
PT	aquaria and waste water.	
XX		
PS	Claim 26; Page 53; 62pp; English.	
XX		
CC	The invention relates to 4 novel types of ammonia-oxidising bacteria	
CC	(AOB) found in freshwater aquaria. The bacteria are able to oxidise	
CC	ammonia to nitrite and are members of the ammonia-oxidising bacteria	
CC	family of the beta subdivision of Proteobacteria. The 4 types of bacteria	
CC	can be distinguished on the basis of their 16S rRNA (ribosomal RNA) gene	

CC sequences (ABA02416-ABA02419), and are classified as AOB type A (e.g.,
 CC Rclone10), type A1 (e.g., Rclone187), type B (e.g., R3clone5) and type
 CC C (e.g., R3clone47). The invention also encompasses isolated 16S rRNA
 CC gene sequences of the ammonia-oxidizing bacteria of the invention.
 CC oligonucleotide probes and primers for the detection of these bacteria,
 CC and compositions comprising the bacteria. The bacteria of the invention
 CC are useful in biological filters for reducing ammonia accumulation in
 CC both freshwater and seawater aquaria. They may also be used in waste
 CC water treatment and in bioremediation processes to reduce the level of
 CC pollution caused by ammonia. The present sequence represents a
 CC specifically claimed probe for the detection of the 16S rRNA gene
 CC sequences of the type A and A1 ammonia-oxidizing bacteria (ABA02416-
 CC ABA02417). (Updated on 29-AUG-2003 to standardise OS field)
 CC XX

SQ Sequence 18 BP; 2 A; 9 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 6; Length 18;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCCCTCTCTGATAC 18
 |||||
 Db 1 CCCCCCTCTCTGATAC 18

RESULT 2

ADM32708
 ID ADM32708 standard; DNA; 18 BP.

AC ADM32708;

DT 17-JUN-2004 (first entry)

XX Nitrospiro-like 16S rDNA probe. S-G-Nespa-0149-a-A-18.

KW 16S rDNA; ammonia oxidizing bacteria; AOB; ammonia; nitrite;
 KW aqueous environment; freshwater; seawater; aquarium; ss; probe.

OS Nitrospiro sp.

XX WO2004026772-A1.

PD 01-APR-2004.

PE 10-SEP-2003; 2003WO-US028210.

XX 19-SEP-2002; 2002US-0386217P.

PR 19-SEP-2002; 2002US-0386218P.

XX 19-SEP-2002; 2002US-0386219P.

PA (AQUA-) AQUARIA INC.

XX Hovanec TA;

DR WPI; 2004-304936/28.

XX New composition comprising an isolated bacterial strain that oxidizes
 XX ammonia to nitrite, useful for alleviating or preventing the accumulation
 PT of ammonia in aqueous environment.
 XX Example 6; Page 34; 98pp; English.

CC This sequence represents a probe which was used in the detection of 16S
 CC rDNA sequence derived from an ammonia oxidizing bacteria (AOB). The
 CC amplified sequence may be used in a composition which comprises an
 CC isolated bacterial strain that oxidizes ammonia to nitrite. The
 CC composition may be used for alleviating or preventing the accumulation of
 CC ammonia in a medium. The ammonia is reduced by at least 30% when compared
 CC with a level of ammonia that would exist in the absence of the bacterial
 CC strain. The composition is useful for alleviating or preventing the
 CC accumulation of ammonia in aqueous environment, e.g. a freshwater or
 CC seawater aquarium.
 CC XX

SQ Sequence 18 BP; 2 A; 9 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 12; Length 18;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCCCTCTCTGATAC 18
 |||||
 Db 1 CCCCCCTCTCTGATAC 18

RESULT 3

AA511828/c
 ID AA511828 standard; DNA; 30 BP.

AC AA511828;

DT 24-OCT-2001 (first entry)

XX Human surfactant protein B, SPB, TTF-1 containing oligonucleotide Bcm.

KW Human surfactant protein B; SPB; promoter; nuclear protein binding site;
 KW thyroid transcription factor; TTF-1; lung cancer; thyroid cancer; ds;

KM Bcm; mutant.

XX Homo sapiens.

OS Synthetic.

XX Location/Qualifiers

FT mutation
 FT /*tag= a
 FT /note= "Mutates the TTF-1 binding site"

PN US2001016352-A1.

PD 23-AUG-2001.

XX 26-MAY-1999; 99US-00320337.

XX 18-MAY-1994; 94US-00245356.

PR 17-MAY-1995; 95US-00442809.

XX (BOHI/) BOHINSKI R J.

PA (WHIT/) WHITSETT J A.

PI Bohinski RJ, Whitsett JA;

XX WPI; 2001-513959/56.

XX Oligonucleotide sequences which bind nuclear proteins and surfactants
 PT found in lung cells, useful for detecting cancers that originate in the
 PT lung.
 XX Example 5; Fig 34a; 76pp; English.

CC The invention relates to an oligonucleotide which includes at least 1
 CC nucleic acid sequence which binds to at least 1 nuclear protein found in
 CC lung cells (e.g. the thyroid transcription factor 1, TTF-1, protein). The
 CC oligonucleotide can be expressed in lung cells via a vector and can be
 CC used to target therapeutic agents to kill lung or thyroid cancer cells.
 CC The oligonucleotide can be used to detect or diagnose lung or thyroid
 CC cancer. The oligonucleotides may be designed from the sequences of, for
 CC example, the promoters of lung-specific genes such as those encoding
 CC surfactant proteins. The present sequence is a mutated oligonucleotide
 CC from human surfactant protein B, SPB, promoter used in an EMSA
 CC (electrophoretic mobility shift assay) assay to confirm the presence of
 CC TTF-1 binding sites in the SPB promoter. The TTF-1 site has been mutated
 CC XX

SQ Sequence 30 BP; 6 A; 6 C; 12 G; 6 T; 0 U; 0 Other;
 Query Match 80.0%; Score 14.4; DB 4; Length 30;
 Best Local Similarity 93.8%; Pred. No. 2.6e+03;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 CCCCCCTCTCGATA 17
 |||||
 DB 24 CCCCCCTCTCGATA 9

RESULT 4

ADM32724
 ID ADM32724 standard; DNA; 18 BP.

AC ADM32724;

DT 17-JUN-2004 (first entry)

DE Nitrosomonas aestuarii-like 16S rDNA probe.

KW 16S rDNA; ammonia oxidizing bacteria; AOB; ammonia; nitrite;
 aqueous environment; freshwater; seawater; aquarium; ss; probe.

OS Nitrosomonas aestuarii.

PN WO2004026772-A2.

PD 01-APR-2004.

PF 10-SEP-2003; 2003WO-US028210.

PR 19-SEP-2002; 2002US-0386217P.

PR 19-SEP-2002; 2002US-0386218P.

PR 19-SEP-2002; 2002US-0386219P.

PA (AQUA-) AQUARIA INC.

PI Hovanec TA;

DR WPI; 2004-304936/28.

PT New composition comprising an isolated bacterial strain that oxidizes
 ammonia to nitrite, useful for alleviating or preventing the accumulation

PT of ammonia in aqueous environment.

PS Claim 10; Page 34; 98pp; English.

CC This sequence represents a probe which was used in the detection of 16S

CC rDNA sequence derived from an ammonia oxidizing bacteria (AOB). The

CC amplified sequence may be used in a composition which comprises an

CC isolated bacterial strain that oxidizes ammonia to nitrite. The

CC composition may be used for alleviating or preventing the accumulation of

CC ammonia in a medium. The ammonia is reduced by at least 30% when compared

CC with a level of ammonia that would exist in the absence of the bacterial

CC strain. The composition is useful for alleviating or preventing the

CC accumulation of ammonia in aqueous environment, e.g. a freshwater or

CC seawater aquarium.

CC

CC

CC

CC

CC

CC

DE PCR primer for human xylosyltransferase (XT) isoform XT-1 cDNA.

KW UDP-xylose:proteoglycan core protein beta-D-xylosyltransferase, XT;

KW XT-I; XT-II; glycosaminoglycan; sclerotic disease; PCR primer;

KW chronic inflammatory joint disease; diagnostic marker; gene marker; ss.

OS Homo sapiens.

PN WO200149831-A2.

PD 12-JUL-2001.

PF 28-DEC-2000; 2000WO-EP013311.

PR 30-DEC-1999; 99EP-00126194.

PR 01-DEC-2000; 2000EP-00126233.

PA (KLESE/) KLESEIEK K.

PI Kleesiek K, Brinkmann T, Goetting C, Kuhn J;

DR WPI; 2001-441872/47.

PT UDP-xylose:proteoglycan core protein beta-D-xylosyltransferase and the

PT nucleic acids that encode it, useful for preventing, diagnosing and

PT treating sclerotic diseases and chronic inflammatory joint diseases.

PS Example 20; Page 29; 80pp; English.

CC The present sequence represents a PCR primer for a cDNA fragment encoding

CC an isoform of UDP-xylose:proteoglycan core protein beta-D-

CC xylosyltransferase (XT). The XT enzyme occurs in at least two isoforms

CC (XT-I) and (XT-II). XT is involved in the biosynthesis of

CC glycosaminoglycans. XT polypeptides and polynucleotides may be used in

CC the production of an agent (inhibitors and antagonists of XT) for the

CC treatment of sclerotic diseases and chronic inflammatory joint diseases,

CC or as a diagnostic marker. The XT DNA may be used as a gene marker. Anti-XT

CC antibodies are used as a diagnostic tool in a immunological assay for

CC detection of a protein having XT activity

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

Sequence 28 BP; 7 A; 2 C; 15 G; 4 T; 0 U; 0 Other;

Query Match 76.7%; Score 13.8; DB 4; Length 28;

Best Local Similarity 88.2%; Pred. No. 5.2e+03; Mismatches 2; Indels 0; Gaps 0;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 CCCCCCTCTCGATA 18

DB 21 CCCCCCTCTCGATA 5

RESULT 6

ADM32573

AC ADM32573;

DT 03-JUN-2004 (first entry)

DE Human carbonic anhydrase II forward PCR primer SEQ ID NO:31.

KW detection; cancer; 8q22.3; chromosome 8; human; EBD; tumor suppressor;

KW cell cycle modulator; DNA repair; DNA damage; nuclear targeting protein;

KW progesterone receptor; cytosolic; gene therapy; squamous cell carcinoma;

KW hepatocellular carcinoma; ovarian cancer; breast cancer; melanoma;

KW head and neck cancer; adenocarcinoma; squamous lung cancer;

KW gastrointestinal cancer; renal cell cancer; bladder cancer;

KW prostate cancer; non-squamous carcinoma; glioblastoma; medullablastoma;

KW carbonic anhydrase II; PCR; primer; ss.

PN WO2004022750-A1.
XX 18-MAR-2004.
PD
XX 05-SEP-2003; 2b03wo-AU001164.
XX 05-SEP-2002; 2002AU-00951346.
XX 07-NOV-2002; 2002US-0425218P.
XX (GARV-) GARVAN INST MEDICAL RES.
PA
PI Watis C, Saunders D, Henderson M, Clancy J, Henshall S;
PI Sutherland R, O'Brien P;
PI
XX WPI; 2004-248472/23.
DR
XX Detecting a cancer cell in a subject sample, also related to cancer
FT treatments, comprises determining the level of nucleic acid that is
PT linked to map position 8q22.3 of the human genome or its expression
PT product.
XX
XX Example 1; SEQ ID NO 31; 331pp; English.

XX The present invention describes a method for detecting a cancer cell in a
XX subject, which comprises determining the level of nucleic acid that is
XX linked to map position 8q22.3 of the human genome or its expression
XX product in a sample of the subject, where an elevated level of the
XX nucleic acid or polypeptide is indicative of cancer in the subject. Also
XX described: (1) a method for diagnosing a cancer or predicting recurrence
XX of a cancer in a subject comprising determining the level of mRNA or
XX protein encoded by a nucleic acid as described above; (2) the isolated or
XX nucleic acid molecule for detecting cancer cell; (3) an isolated or
XX recombinant protein complex; (4) an antibody that binds to the protein
XX complex; (5) a kit for detecting or producing a protein complex
XX comprising an EDD polypeptide or a portion of an EDD polypeptide and a
XX second polypeptides selected from a protein having tumour suppressor
XX activity, a protein having cell cycle regulatory activity, a protein
XX associated with DNA repair or damage, a nuclear targeting protein, and a
XX progesterone receptor protein or its portion, where the portion of the
XX second polypeptide is sufficient to bind to the EDD polypeptide or the
XX portion of an EDD polypeptide; (6) methods for isolating the protein
XX complex; (7) a method for determining a predisposition for disease, or
XX disease state; (8) a method for determining a modulator of the activity,
XX formation or stability of an isolated or recombinant protein complex; (9)
XX a method for determining a modulator of the level of protein complex
XX formation; (10) a method for treating a condition associated with
XX elevated expression of EDD protein in a cell; (11) an antisense nucleic
XX acid, ribozyme, peptide nucleic acid (PNA), interfering RNA or siRNA; and
XX (12) a pharmaceutical composition comprising the antisense nucleic acid,
XX ribozyme, PNA, interfering RNA or siRNA. EDD has cytostatic activity, and
XX can be used in gene therapy. The methods and modulator are useful for
XX treating a condition associated with EDD over expression such as cancer,
XX e.g. squamous cell carcinoma, hepatocellular carcinoma, ovarian cancer,
XX breast cancer, melanoma, head and neck cancer, adenocarcinoma, squamous
XX lung cancer, gastrointestinal cancer (e.g. gastric, colon, or pancreatic
XX cancer), renal cell cancer, bladder cancer, prostate cancer, non-squamous
XX carcinoma, glioblastoma and medulloblastoma. The components and
XX composition are useful for reducing the expression of EDD in a cell to
XX inhibit cellular proliferation. The present sequence represents a PCR
XX primer for human carbonic anhydrase II, which is used in the
XX exemplification of the present invention.

XX Sequence 22 BP; 3 A; 10 C; 3 G; 6 T; 0 U; 0 Other;

QY Query Match 74.4%; Score 13.4; DB 12; Length 22;
Best Local Similarity 93.3%; Pred. No. 8.1e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCCCCCTCTTGGA 15
DB 5 CCCTCCTCTTGGA 19

RESULT 7
AD36420/c
ID ADC36420 standard; DNA; 20 BP.
XX
XX
XX AD36420;
AC
XX
XX 18-DEC-2003 (first entry)
DT
XX
XX Weed controller metabolism associated PCR primer SEQ ID NO:288.
DE
XX
XX Weed controller metabolism; weed; herbicide; herbicide-resistant plant;
KW agrochemical; ss; PCR; primer.
XX
XX
XX Synthetic.
OS
XX
XX WO2003040370-A1.
PN
XX
XX 15-MAY-2003.
PD
XX
XX 17-OCT-2002; 2002WO-JP010789.
PP
XX
XX 19-OCT-2001; 2001JP-00321307.
PR
XX 07-JUN-2002; 2002JP-00167239.
XX
XX (SDMO) SUMITOMO CHEM CO LTD.
PA
XX
XX Nakajima H, Mukumoto F, Takashi M;
PI
XX WPI; 2003-523102/49.
DR

XX Weed controller metabolism proteins deactivating porphyrinogen oxidase
PT (PPO)-inhibiting herbicides by N-demethylation and their genes, useful
PT e.g. in constructing new breeds of herbicide-resistant plants.
XX
XX Disclosure; SEQ ID NO 288; 812pp; Japanese.

XX The invention relates to a novel DNA encoding a weed controller
XX metabolism protein. A protein of the invention has herbicide activity.
XX The proteins and their encoded genes are useful e.g. in constructing new
XX breeds of herbicide-resistant plants and also in developing various
XX agrochemicals. The present sequence is used in the exemplification of the
XX invention.

XX Sequence 20 BP; 5 A; 4 C; 8 G; 3 T; 0 U; 0 Other;

QY Query Match 73.3%; Score 13.2; DB 10; Length 20;
Best Local Similarity 83.3%; Pred. No. 1e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCCCCTCTTGATAC 18
DB 18 CCACCGTCTCTGATAC 1

RESULT 8
AD331445/c
ID AD331445 standard; DNA; 27 BP.
XX
XX
XX AD331445;
AC
XX
XX 26-FEB-2004 (first entry)
DT
XX
XX PCR primer used to amplify human c-erbB2 DNA SeqID 113.
DE
XX
XX human; PCR; ss; primer; MN/CA IX; MN; oncogene; carbonic anhydrase 9;
KW CA9; MN/CA9; carbonic anhydrase IX; CA IX; MN/9250; neoplastic tumour;
KW cytostatic; cancer; tumour therapy; anti-tumour vaccine.
XX
XX
XX Homo sapiens.
OS
XX
XX WO2003100029-A2.
PN
XX
XX 04-DEC-2003.
PD

XX 22-FEB-2003; 2003WO-US005136.
XX
XX 23-MAY-2002; 2002US-0383068P.
XX 05-DEC-2002; 2002US-0431499P.
XX
XX (FARB) BAYER CORP.
XX (VIRO-) INST VIROLOGY.
XX
XX Pastorek J, Pastorekova S, Zlatovicova M, Zavada J, Ortova Gut M;
XX WPI; 2004-035136/03.
XX
XX New monoclonal antibody generated from MN/CA IX-deficient mice, where the
XX antibody binds specifically to human tumor-associated cell adhesion
XX protein MN/CA IX or polypeptide, useful for diagnosing, prognosing or
XX treating cancer.
XX
XX Example 11; SEQ ID NO 113; 156pp; English.
XX
XX This invention relates to a novel monoclonal antibody identified as the
XX MN/CA IX specific antibody prepared in knockout mice (CA IX deficient
XX mice). Specifically, this antibody is directed towards the MN gene, a
XX cellular oncogene known alternatively as carbonic anhydrase 9, CA9 or
XX MN/CA9, which encodes the MN protein that is also known as the MN/CA IX
XX isoenzyme, carbonic anhydrase IX, CA IX or the MN/G250 protein. The
XX present invention describes the generation of this monoclonal antibody,
XX and immunoreactive fragments thereof, which are directed against non-
XX immunodominant epitopes on the CA IX extracellular domain. As such, this
XX antibody can be useful diagnostically as a marker for preneoplastic/
XX neoplastic tumours, immunodetection methods and immunotargeting
XX approaches. Accordingly, compositions exhibit cytostatic activity and are
XX useful in the diagnosis, prognosis and treatment of various cancers
XX including breast, bladder or lung cancer, in tumour therapy and in anti-
XX tumour vaccination. This oligonucleotide sequence is an PCR primer used
XX to amplify DNA of a human breast tumour marker, in an exemplification of
XX the invention.
XX
XX Sequence 27 BP; 6 A; 6 C; 10 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 73.3%; Score 13.2; DB 12; Length 27;
XX Best Local Similarity 83.3%; Pred. No. 1e+04;
XX Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 1 CCCCCCTCTCTGGAATAC 18
XX DB 19 CCTCTCATCTGGAAC 2
XX
XX RESULT 9
XX ADK41856/c
XX ID ADK41856 standard; DNA; 27 BP.
XX
XX ADK41856;
XX
XX 06-MAY-2004 (first entry)
XX
XX Human MN gene-related PCR primer SeqID109.
XX
XX carbonic anhydrase IX; CA IX; precancerous cell; MN; cancerous cell;
XX human; vertebrate; cytostatic; vaccine; gene therapy;
XX renal cell carcinoma; breast cancer; colorectal cancer; PCR; primer; ss.
XX
XX Homo sapiens.
XX
XX WO2004005348-A1.
XX
XX 15-JAN-2004.
XX
XX 22-FEB-2003; 2003WO-US005137.
XX
XX 23-MAY-2002; 2002US-0383068P.
XX
XX 05-DEC-2002; 2002US-0431499P.
XX

XX (FARB) BAYER CORP.
XX (VIRO-) INST VIROLOGY.
XX
XX Zavada J, Pastorekova S, Pastorek J, Zavadova Z;
XX WPI; 2004-083500/08.
XX
XX New soluble form of the carbonic anhydrase IX (CA IX) protein for
XX screening, diagnosing or prognosing diseases associated with abnormal
XX expression of CA IX protein, e.g. renal cell carcinoma, breast cancer or
XX colorectal cancer.
XX
XX Example 11; SEQ ID NO 113; 159pp; English.
XX
XX This invention relates to a novel soluble form of the carbonic anhydrase
XX IX (CA IX) (or MN) protein or CA IX polypeptide which is released from
XX precancerous and/or cancerous cells of a vertebrate into a body fluid.
XX The invention may be useful for the development of compounds with a
XX cytostatic activity or a vaccine whilst the disclosed sequences may be
XX used for gene therapy. The protein and method are useful for screening,
XX diagnosing or prognosing diseases associated with abnormal expression of
XX carbonic anhydrase IX protein, such as precancerous and cancerous
XX diseases like renal cell carcinoma, breast cancer or colorectal cancer.
XX The monoclonal antibody may also be used for treating or preventing
XX precancerous and cancerous diseases. The present sequence is that of a
XX PCR primer which was used in the exemplification of the invention.
XX
XX Sequence 27 BP; 6 A; 6 C; 10 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 73.3%; Score 13.2; DB 12; Length 27;
XX Best Local Similarity 83.3%; Pred. No. 1e+04;
XX Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 1 CCCCCCTCTCTGGAATAC 18
XX DB 19 CCTCTCATCTGGAAC 2
XX
XX RESULT 10
XX ADC36414
XX ID ADC36414 standard; DNA; 28 BP.
XX
XX ADC36414;
XX
XX 18-DEC-2003 (first entry)
XX
XX Weed controller metabolism associated PCR primer SEQ ID NO:282.
XX
XX weed controller metabolism; weed; herbicide; herbicide-resistant plant;
XX agrochemical; ss; PCR; primer.
XX
XX Synthetic.
XX
XX WO2003040370-A1.
XX
XX 15-MAY-2003.
XX
XX 17-OCT-2002; 2002WO-JP010789.
XX
XX 19-OCT-2001; 2001JP-00321307.
XX
XX 07-JUN-2002; 2002JP-00167239.
XX
XX (SUMO) SUMITOMO CHEM CO LTD.
XX
XX Nakajima H, Mukumoto F, Takaiishi M;
XX WPI; 2003-523102/49.
XX
XX Weed controller metabolism proteins deactivating porphyrinogen oxidase
XX (PPO)-inhibiting herbicides by N-demethylation and their genes, useful
XX e.g. in constructing new breeds of herbicide-resistant plants.
XX

PS Disclosure; SEQ ID NO 282; 812bp; Japanese.
XX
CC The invention relates to a novel DNA encoding a weed controller
CC metabolism protein. A protein of the invention has herbicide activity.
CC The proteins and their encoded genes are useful e.g. in constructing new
CC breeds of herbicide-resistant plants and also in developing various
CC agrochemicals. The present sequence is used in the exemplification of the
CC invention.
XX
SQ Sequence 28 BP; 5 A; 11 C; 7 G; 5 T; 0 U; 0 Other;
XX
Query Match 73.3%; Score 13.2; DB 10; Length 28;
Best Local Similarity 83.3%; Pred. No. 1e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 1 CCCCCCTCTCTGGATAC 18
DB 11 CCACCGTCTCTGGATAC 28
XX
RESULT 11
ACA54549/c
ID ACA54549 standard; DNA; 30 BP.
XX
AC ACA54549;
XX
XX 27-OCT-2003 (revised)
DT 19-JUN-2003 (first entry)
XX
XX Prokaryotic folA gene PCR primer #1.
XX
XX Antisense; ss; prokaryotic essential gene; cell proliferation;
KW drug design; primer; PCR.
XX
XX Archaea.
OS
PN WO200271183-A2.
XX
XX 03-OCT-2002.
PD
XX 21-MAR-2002; 2002WO-US009107.
PF
XX 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
XX (ELIT-) ELITRA PHARM INC.
XX
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Foreysch RA, Xu HH;
XX
XX WPI; 2003-029926/02.
DR
XX
XX New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
XX Example 21; Page 1574; 1766pp; English.
XX
XX The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway

CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation, or to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is a PCR primer used
CC to amplify isolated DNA from an essential gene which, when overexpressed,
CC allows growth in the presence elevated antibiotic concentrations.
XX
XX (Updated on 27-OCT-2003 to standardise OS field)
XX
SQ Sequence 30 BP; 11 A; 3 C; 10 G; 6 T; 0 U; 0 Other;
XX
Query Match 73.3%; Score 13.2; DB 8; Length 30;
Best Local Similarity 83.3%; Pred. No. 1e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 1 CCCCCCTCTCTGGATAC 18
DB 21 CCTCCTTCTCTGGATCC 4
XX
RESULT 12
ABX13526/c
ID ABX13526 standard; DNA; 30 BP.
XX
XX ABX13526;
AC
XX
XX 04-JUN-2003 (first entry)
DT
XX
XX
XX *S. aureus* folA PCR primer SEQ ID 15798.
DE
XX
XX Cellular proliferation; inhibitor; target; primer; PCR; folA;
KW trimethoprim; ss.
XX
XX *Staphylococcus aureus*.
OS
PN WO200286097-A2.
XX
XX 31-OCT-2002.
PD
XX 08-FEB-2002; 2002WO-US003987.
PF
XX 09-FEB-2001; 2001US-0267636P.
PR
XX
XX (ELIT-) ELITRA PHARM INC.
XX
XX Carr GJ, Xu HH, Foulkes GJ, Zamudio C, Haselbeck R, Ohlsen KL;
PI Zyskind JW, Wall D, Trawick JD, Yamamoto RT, Roemer T, Jiang B,
PI Boone C, Bussey H;
XX
XX WPI; 2003-093126/08.
DR
XX
XX Identifying the target of a compound which inhibits cellular
PT proliferation, comprises contacting a culture of strains that overexpress
PT or underexpress a gene product with the above compound, and identifying
PT the gene product.
XX
XX Example 16; Page 315; 640pp; English.
XX
XX This invention describes a novel method for identifying gene products on
CC which compounds inhibiting proliferation of an organism act. The method
CC comprises obtaining a culture of strains overexpressing a different
CC product for proliferation of the organism, contacting the culture with a
CC compound to inhibit proliferation of strains that do not overexpress the

CC product and identifying the product overexpressed in a strain that
CC proliferated more rapidly. The method is useful in identifying the target
CC of a compound which reduces the activity or level of gene products
CC required for cellular proliferation. The method may also be used for
CC identifying the therapeutic compounds that act on the novel targets. This
CC sequence represents a PCR primer used to amplify the *Staphylococcus*
CC *aureus* *folA* gene which is inhibited by trimethoprim

XX
SQ Sequence 30 BP; 11 A; 3 C; 10 G; 6 T; 0 U; 0 Other;

Query Match 73.3%; Score 13.2; DB 8; Length 30;
Best Local Similarity 83.3%; Pred. No. 1e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCCCCTTTCTGGATC 18
DB 21 CCTCCTTCTTGGATCC 4

RESULT 13

ID ADH30251 standard; DNA; 17 BP.

XX ADH30251;

DT 11-MAR-2004 (first entry)

DE Human monocyte-macrophage cell surface apob48 receptor primer #5.

XX antilipemic; gene therapy;

KW monocyte-macrophage cell surface apob48 receptor; apob48r;

KW pattern B phenotype; familial combined hyperlipidaemia;

KW hypercholesterolaemia; hypertriglyceridaemia;

XX low plasma high-density lipoprotein level; human; primer; ss.

OS Homo sapiens.

XX US2003208060-A1.

XX 06-NOV-2003.

XX 12-JUN-2003; 2003US-00459876.

XX 06-AUG-1998; 98US-00130242.

XX 31-MAY-2000; 2000US-00583610.

XX (GIAN/) GIANTURCO S H.

XX (BRAD/) BRADLEY W A.

XX Gianturco SH, Bradley WA;

XX WPI; 2003-864799/80.

XX New isolated DNA molecule encoding a monocyte-macrophage cell surface

XX apob48 receptor protein (apob48r), useful in preparing a composition for

XX treating e.g., familial or non-familial hypercholesterolaemia.

XX Example 23; SEQ ID NO 17; 77pp; English.

XX The invention describes a new isolated DNA molecule, encoding a monocyte-

XX macrophage cell surface apob48 receptor protein (apob48r) comprising a

XX fully defined 1088 amino acid sequence. The DNA molecule is useful in

XX preparing a composition for treating pattern B phenotype, familial

XX combined hyperlipidaemia, familial or non-familial hypercholesterolaemia,

XX hypertriglyceridaemia or low plasma high-density lipoprotein levels. This

XX sequence represents a primer used in the isolation of human monocyte-

XX macrophage cell surface apob48 receptor DNA.

XX Sequence 17 BP; 2 A; 6 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 71.1%; Score 12.8; DB 10; Length 17;

Best Local Similarity 87.5%; Pred. No. 1.6e+04;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCCCCCTTTCTGGAT 16
DB 1 CCAGCCTTCTGGAT 16

RESULT 14

ID ADO00840 standard; DNA; 17 BP.

XX ADO00840;

DT 12-AUG-2004 (first entry)

DE Human monocyte-macrophage cell surface apob48r cDNA PCR primer #6.

XX Human; monocyte-macrophage cell surface apolipoprotein B 48 receptor;

KW apolipoprotein B 48 receptor; apob48r; PCR; ss; monocyte; macrophage;

KW reticuloendothelial cell; monocyte adhesion; cardiovascular disease;

KW apob-mediated cellular uptake; plasma chylomicron;

KW hypertriglyceridaemic triglyceride-rich lipoprotein;

KW Apob independent pathway; lipoprotein lipase independent pathway;

KW heparin sulfate proteoglycan independent pathway; foam cell formation;

XX hypertriglyceridaemia; primer.

OS Homo sapiens.

XX US6740735-B1.

XX 25-MAY-2004.

XX 31-MAY-2000; 2000US-00583610.

XX 06-AUG-1998; 98US-00130242.

XX (GIAN/) GIANTURCO S H.

XX (BRAD/) BRADLEY W A.

XX Gianturco SH, Bradley WA;

XX WPI; 2004-387250/36.

XX New isolated monocyte-macrophage cell surface apob48 receptor protein,

XX useful for cell-specific delivery of therapeutic compounds to human

XX monocytes or macrophages, or for evaluating an individual at risk for

XX cardiovascular disease.

XX Example 23; SEQ ID NO 17; 72pp; English.

XX The invention relates to the human monocyte-macrophage cell surface

XX apolipoprotein B 48 receptor (apob48r) protein and the nucleic acid

XX encoding it. The invention also relates to a method of cell-specific

XX delivery of therapeutic compounds to human monocytes, macrophages or

XX other reticuloendothelial cells that express the receptor, a method of

XX inhibiting foam cell formation and increased monocyte adhesion to

XX endothelial cells and a method of evaluating an individual at risk of a

XX cardiovascular disease. The monocyte-macrophage cell surface apob48

XX receptor protein is useful in the apob-mediated cellular uptake of plasma

XX chylomicrons and remnants and hypertriglyceridaemic triglyceride-rich

XX lipoproteins in an Apob independent pathway, a lipoprotein lipase

XX independent pathway or a heparin sulfate proteoglycan independent

XX pathway. It is also useful for the cell-specific delivery of therapeutic

XX compounds to human monocytes, macrophages or other reticuloendothelial

XX cells that express the receptor, for inhibiting foam cell formation and

XX increased monocyte adhesion to endothelial cells and for evaluating an

XX individual at risk of a cardiovascular disease such as

XX hypertriglyceridaemia. This sequence represents a PCR primer used in

XX cloning of cDNA encoding the apob48r protein of the invention.

XX Sequence 17 BP; 2 A; 6 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 71.1%; Score 12.8; DB 12; Length 17;

Best Local Similarity 87.5%; Pred. No. 1.6e+04;

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 6, 2006, 14:55:23 ; Search time 102.614 Seconds
(without alignments)
10525.104 Million cell updates/sec

Title: US-10-659-980A-8

Perfect score: 19
Sequence: 1 tccccctcgaagatcacg 19

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenBml: *
1: gb_ba: *
2: gb_in: *
3: gb_env: *
4: gb_om: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pr: *
9: gb_ro: *
10: gb_sts: *
11: gb_sy: *
12: gb_un: *
13: gb_vl: *
14: gb_htg: *
15: gb_pl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	100.0	19	6	CQ796915 Sequence
2	19	100.0	19	6	CS089161 Sequence
3	19	100.0	19	6	AX316099 Sequence
4	19	100.0	428	3	AF134441 Unculture
5	19	100.0	455	3	AF134442 Unculture
6	19	100.0	493	3	AY921481 Unculture
7	19	100.0	983	1	AF408634 Nitroscop
8	19	100.0	1207	1	NSP29724 Nitroscop
9	19	100.0	1368	1	NSA168 Nitroscop
10	19	100.0	1378	1	NTV16RNNAA Nitroscop
11	19	100.0	1388	1	NS168AV Nitroscop
12	19	100.0	1435	1	NTV16SRNNA Nitroscop
13	19	100.0	1469	3	AF386755 Nitroscop
14	19	100.0	1486	3	AF386754 Nitroscop
15	19	100.0	1495	1	AF856079 Nitroscop
16	19	100.0	1497	1	AY123803 Nitroscop
17	19	100.0	1497	1	AY123812 Nitroscop
18	17.4	91.6	550	3	AY283110 Unculture

c 19	17.4	91.6	569	3	AJ704699 Unculture
c 20	17.4	91.6	692	3	AY534019 Unculture
c 21	17.4	91.6	1206	1	AY727034 Nitroscop
c 22	17.4	91.6	1207	1	NSP298747 Nitroscop
c 23	17.4	91.6	1207	1	NTB298746 Nitroscop
c 24	17.4	91.6	1207	1	AY727033 Nitroscop
c 25	17.4	91.6	1217	3	AY726896 Unculture
c 26	17.4	91.6	1285	3	USO390469 Unculture
c 27	17.4	91.6	1294	1	NSA15543 Nitroscop
c 28	17.4	91.6	1319	1	NSA15544 Nitroscop
c 29	17.4	91.6	1321	1	NSA15545 Nitroscop
c 30	17.4	91.6	1399	1	NSL15168 Nitroscop
c 31	17.4	91.6	1434	1	NTV16RNNAB Nitroscop
c 32	17.4	91.6	1442	1	AF353158 Nitroscop
c 33	17.4	91.6	1445	1	AF353157 Nitroscop
c 34	17.4	91.6	1447	1	AF080256 Nitroscop
c 35	17.4	91.6	1448	1	NTV16SRNNA Nitroscop
c 36	17.4	91.6	1457	1	AF353162 Nitroscop
c 37	17.4	91.6	1458	1	AY684260 Nitroscop
c 38	17.4	91.6	1458	6	CQ796910 Sequence
c 39	17.4	91.6	1458	6	CS089156 Sequence
c 40	17.4	91.6	1458	6	AX316094 Sequence
c 41	17.4	91.6	1474	1	NS168R Nitroscop
c 42	17.4	91.6	1486	3	AF386756 Nitroscop
c 43	17.4	91.6	1492	3	AY218727 Unculture
c 44	17.4	91.6	1492	3	AY218730 Unculture
c 45	17.4	91.6	1493	3	AY218755 Unculture

ALIGNMENTS

RESULT 1	CQ796915	19 bp	DNA	linear	PAT 19-APR-2004
LOCUS	CQ796915	Sequence 8 from Patent WO2004026772.			
DEFINITION	CQ796915				
ACCESSION	CQ796915.1	GI:46408541			
VERSION					
KEYWORDS					
SOURCE					
ORGANISM					
synthetic construct					
synthetic construct					
other sequences; artificial sequences.					
REFERENCE					
1	Hovanc,T.A.				
Ammonia-oxidizing bacteria and methods of using and detecting					
thesame					
JOURNAL	Patent: WO 2004026772-A 8 01-APR-2004;				
Aquaria Inc. (US)					
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/mol_type="unassigned DNA"					
/db_xref="taxon:32630"					
/note="Oligonucleotide probe"					
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Best local similarity	100.0%;	Pred. No. 20;			
Matches 19;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	1	TCCTCCCTCGAAGATACG	19		
DB	1	TCCTCCCTCGAAGATACG	19		
RESULT 2	CS089161	19 bp	DNA	linear	PAT 25-MAY-2005
LOCUS	CS089161	Sequence 8 from Patent EP1502948.			
DEFINITION	CS089161				
ACCESSION	CS089161.1	GI:66714445			
VERSION					
KEYWORDS					
SOURCE					
synthetic construct					

ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Hovanec, T.A. and Burrell, P.C.
TITLE Ammonia-oxidizing bacteria
JOURNAL Patent: EP 1502948-A 8 02-FEB-2005;
Aguaria Inc. (US)

FEATURES
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1. .19
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Description of Artificial Sequence: Probe"

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Best Local Similarity 100.0%; Pred. No. 20;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCCCCACTCGAAGATACG 19
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1 TCCCCCACTCGAAGATACG 19

RESULT 3
LOCUS AX316099 19 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 8 from Patent WO0190312.
AX316099
VERSION AX316099.1 GI:17899290
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Hovanec, T.A. and Burrell, P.C.
TITLE Ammonia-oxidizing bacteria
JOURNAL Patent: WO 0190312-A 8 29-NOV-2001;
AQUARIA, INC. (US)

FEATURES
source
1. .19
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Probe"

ORIGIN

Query Match 100.0%; Score 19; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCCCCACTCGAAGATACG 19
1 |||||||
1 TCCCCCACTCGAAGATACG 19

RESULT 4
LOCUS AF134441/c 428 bp rRNA linear ENV 11-MAY-2004
DEFINITION Uncultured beta proteobacterium b4 16S ribosomal RNA, partial
sequence.
ACCESSION AF134441
VERSION AF134441.1 GI:4836726
KEYWORDS ENV.
SOURCE uncultured beta proteobacterium b4
ORGANISM Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
Nitrosomonadaceae; environmental samples.
1 (bases 1 to 428)
REFERENCE Whitby, C.B., Saunders, J.R., Rodriguez, J., Pickup, R.W. and
AUTHORS McCarthy, A.
TITLE Phylogenetic differentiation of two closely related Nitrosomonas
 spp. That inhabit different sediment environments in an

JOURNAL Appl. Environ. Microbiol. 65 (11), 4855-4862 (1999)
PUBMED 10543796
REFERENCE 2 (bases 1 to 428)
AUTHORS Whitby, C.W., Saunders, J.R., Rodriguez, J., Pickup, R.W. and
McCarthy, A.J.
TITLE Direct Submission
JOURNAL Submitted (12-MAR-1999) School of Biological Sciences, University
of Liverpool, Crown Street, Liverpool, Merseyside L69 7ZB, UK

FEATURES
source
1. .428
/organism="uncultured beta proteobacterium b4"
/mol_type="rRNA"
/db_xref="taxon:93622"
/chromosome="1"
/clone="b4"
/environmental sample
/note="similar to Escherichia coli locus UBd4"
/product="16S ribosomal RNA"

ORIGIN

Query Match 100.0%; Score 19; DB 3; Length 428;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCCCCACTCGAAGATACG 19
1 |||||||
63 TCCCCCACTCGAAGATACG 45

RESULT 5
LOCUS AF134442/c 455 bp rRNA linear ENV 11-MAY-2004
DEFINITION Uncultured beta proteobacterium b5 16S ribosomal RNA, partial
sequence.
ACCESSION AF134442
VERSION AF134442.1 GI:4836727
KEYWORDS ENV.
SOURCE uncultured beta proteobacterium b5
ORGANISM Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
Nitrosomonadaceae; environmental samples.
1 (bases 1 to 455)
REFERENCE Whitby, C.B., Saunders, J.R., Rodriguez, J., Pickup, R.W. and
AUTHORS McCarthy, A.
TITLE Phylogenetic differentiation of two closely related Nitrosomonas
 spp. That inhabit different sediment environments in an
oligotrophic freshwater lake
JOURNAL Appl. Environ. Microbiol. 65 (11), 4855-4862 (1999)
PUBMED 10543796
REFERENCE 2 (bases 1 to 455)
AUTHORS Whitby, C.W., Saunders, J.R., Rodriguez, J., Pickup, R.W. and
McCarthy, A.J.
TITLE Direct Submission
JOURNAL Submitted (12-MAR-1999) School of Biological Sciences, University
of Liverpool, Crown Street, Liverpool, Merseyside L69 7ZB, UK

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/mol_type="rRNA"
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/clone="b5"
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/note="similar to Escherichia coli locus UBd4"
/product="16S ribosomal RNA"

ORIGIN

Query Match 100.0%; Score 19; DB 3; Length 455;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 TCCCCCACTCGAAGATACG 19
Db      28 TCCCCCACTCGAAGATACG 10

RESULT 6
LOCUS   AY921481
DEFINITION Uncultured bacterium clone AF5 16S ribosomal RNA gene, partial
sequence.
ACCESSION AY921481
VERSION   AY921481.1
KEYWORDS ENV.
SOURCE   uncultured bacterium
ORGANISM Bacteria; environmental samples.
REFERENCE 1 (bases 1 to 493)
AUTHORS  Ka,J.-O., Jung,M.-K., Kim,M.-S. and Ahn,J.-H.
TITLE    Changes in bacterial community in rice field soils
JOURNAL  Unpublished
REFERENCE 2 (bases 1 to 493)
AUTHORS  Ka,J.-O., Jung,M.-K., Kim,M.-S. and Ahn,J.-H.
TITLE    Direct Submision
JOURNAL  Submitted (06-FEB-2005) School of Applied Biology and Chemistry,
Seoul National University, San 56-1 Sillindong Kwanakgu, Seoul
151-921, Korea
FEATURES
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         1..493
         /organism="uncultured bacterium"
         /mol_type="genomic DNA"
         /isolation_source="rice field soil"
         /db_xref="taxon:77133"
         /clone="AF5"
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         /product="16S ribosomal RNA"

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Query Match      100.0%; Score 19; DB 3; Length 493;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TCCCCCACTCGAAGATACG 19
Db      365 TCCCCCACTCGAAGATACG 383

RESULT 7
LOCUS   AF408634/c
DEFINITION Nitrosospirota multiformis strain 24C 16S ribosomal RNA gene, partial
sequence.
ACCESSION AF408634
VERSION   AF408634.1
KEYWORDS GI:16139825
SOURCE   Nitrosospirota multiformis
ORGANISM Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
          Nitrosospirota multiformis;
          Nitrosomonadaceae; Nitrosospirota.
REFERENCE 1 (bases 1 to 983)
AUTHORS  Norton,J.M., Alzerreca,J.J., Suwa,Y. and Klotz,M.G.
TITLE    Diversity of the amo operon in autotrophic ammonia-oxidizing
bacteria
JOURNAL  Unpublished
REFERENCE 2 (bases 1 to 983)
AUTHORS  Norton,J.M. and Klotz,M.G.
TITLE    Direct Submission
JOURNAL  Submitted (10-AUG-2001) Plant, Soils and Biometeorology, Utah State
University, 4820 Old Main Hill, Logan, UT 84322, USA
FEATURES
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         1..983
         /organism="Nitrosospirota multiformis"

Qy      1 TCCCCCACTCGAAGATACG 19
Db      28 TCCCCCACTCGAAGATACG 10

RESULT 8
LOCUS   NSP298724/c
DEFINITION Nitrosospirota sp. 24C partial 16S rRNA gene, isolate 24C.
ACCESSION AJ298724
VERSION   AJ298724.1
KEYWORDS 16S ribosomal RNA; 16S rRNA gene.
SOURCE   Nitrosospirota sp. 24C
ORGANISM Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
          Nitrosomonadaceae; Nitrosospirota.
REFERENCE 1
AUTHORS  Aakra,A., Utaker,J.B., Pommeroy-Roser,A., Koops,H.P. and
Nes,I.P.
TITLE    Detailed phylogeny of ammonia-oxidizing bacteria determined by rDNA
sequences and DNA homology values
JOURNAL  Int. J. Syst. Evol. Microbiol. 51 (Pt 6), 2021-2030 (2001)
REFERENCE 2 (bases 1 to 1207)
AUTHORS  Aakra,A.
TITLE    Direct Submission
JOURNAL  Submitted (30-AUG-2000) Aakra A., Laboratory of Microbial Gene
Technology, Agricultural University of Norway, P.O. Box 5051,
N-1432 Aas, NORWAY
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         /organism="Nitrosospirota sp. 24C"
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         /gene="16S rRNA"
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Best Local Similarity 100.0%; Pred. No. 18;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TCCCCCACTCGAAGATACG 19
Db      23 TCCCCCACTCGAAGATACG 5

RESULT 9
LOCUS   NSAP16S/c
DEFINITION Nitrosospirota sp. 16S rRNA gene, isolate AF.
ACCESSION X84658
VERSION   X84658.1
KEYWORDS 16S ribosomal RNA.
SOURCE   Nitrosospirota sp.
ORGANISM Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
```

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
SOURCE
ORIGIN

1 Nitrosomonadaceae; Nitrospira.
Utaker, J.B., Bakken, L., Jiang, Q.Q. and Nes, I.F.
Phylogenetic analysis of seven new isolates of the highly related ammonia-oxidizing bacteria based on 16S rRNA gene sequencing
Syst. Appl. Microbiol. 18, 549-559 (1995)
2 (bases 1 to 1368)
Utaker, J.B.
Direct Submission
Submitted (09-FEB-1995) J.B. Utaker, Agricultural University of Norway, Lab of Microbial Gene Technology, PO Box 5051, 1432 Aas
NLH, NORWAY
Location/Qualifiers
1..1368
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/db_xref="taxon:38080"
<1..>1368
/product="16S ribosomal RNA"

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Best Local Similarity 100.0%; Pred. No. 18;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCCCCACTCGAAGATACG 19
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Db 90 TCCCCCACTCGAAGATACG 72

RESULT 10
NTV16SRNA/c
LOCUS NTV16SRNA 1378 bp DNA linear BCT 12-OCT-1993
DEFINITION Nitrosovibrio tenuis 16S ribosomal RNA (16S rRNA) gene sequence.
ACCESSION M96404
VERSION M96404.1 GI:150439
KEYWORDS 16S ribosomal RNA.
SOURCE Nitrosovibrio tenuis
ORGANISM Nitrosovibrio tenuis
Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
Nitrosomonadaceae; Nitrosovibrio.
1 (bases 1 to 1378)
Head, I.M., Hiorns, W.D., Embley, T.M., McCarthy, A.J. and
Saunders, J.R.
The phylogeny of autotrophic ammonia-oxidizing bacteria as
determined by analysis of 16S ribosomal RNA gene sequences
J. Gen. Microbiol. 139 (Pt 6), 1147-1153 (1993)
COMMENT
PUBMED 7689633
Original source text: Nitrosovibrio tenuis (strain Nv1) DNA.
FEATURES
source
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/mol_type="unassigned DNA"
/db_xref="taxon:1233"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 18;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCCCCACTCGAAGATACG 19
|||||
Db 124 TCCCCCACTCGAAGATACG 106

RESULT 11
NS16SAV/c
LOCUS NS16SAV 1388 bp DNA linear BCT 19-DEC-2002
DEFINITION Nitrospira sp. NPAV partial 16S rRNA gene, strain NPAV.
ACCESSION Y10127
VERSION Y10127.2 GI:27262953
KEYWORDS 16S ribosomal RNA; 16S rRNA gene.

SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
REMARK
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
SOURCE

Nitrospira sp. NPAV
Nitrospira sp. NPAV
Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
Nitrosomonadaceae; Nitrospira.
1
McCaig, A.E., Embley, T.M. and Prosser, J.I.
Molecular analysis of enrichment cultures of marine ammonia
oxidisers
FEMS Microbiol. Lett. 120 (3), 363-367 (1994)
8076810
2
Prosser, J., Freitag, T. and Smith, Z.
1
Unpublished
3
McCaig, A.E.
Direct Submission
Submitted (18-DEC-1996) A.E. McCaig, Institute of Medical Sciences,
Molecular and Cell Biology, University of Aberdeen, Foresterhill,
Aberdeen, AB25 2ZD, UK
revised by [4]
4 (bases 1 to 1388)
McCaig, A.E.
Direct Submission
Submitted (08-NOV-2002) A.E. McCaig, Institute of Medical Sciences,
Molecular and Cell Biology, University of Aberdeen, Foresterhill,
Aberdeen, AB25 2ZD, UK
On Dec 19, 2002 this sequence version replaced gi.1771383.
Location/Qualifiers
1..1388
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/product="16S ribosomal RNA"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 18;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCCCCACTCGAAGATACG 19
|||||
Db 57 TCCCCCACTCGAAGATACG 39

RESULT 12
NTV16SRNA/c
LOCUS NTV16SRNA 1435 bp DNA linear BCT 12-OCT-1993
DEFINITION Nitrosovibrio tenuis 16S ribosomal RNA (16S rRNA) gene sequence.
ACCESSION M96397
VERSION M96397.1 GI:150441
KEYWORDS 16S ribosomal RNA.
SOURCE Nitrosovibrio tenuis
ORGANISM Nitrosovibrio tenuis
Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
Nitrosomonadaceae; Nitrosovibrio.
1 (bases 1 to 1435)
Head, I.M., Hiorns, W.D., Embley, T.M., McCarthy, A.J. and
Saunders, J.R.
The phylogeny of autotrophic ammonia-oxidizing bacteria as
determined by analysis of 16S ribosomal RNA gene sequences
J. Gen. Microbiol. 139 (Pt 6), 1147-1153 (1993)
COMMENT
PUBMED 7689633
Original source text: Nitrosovibrio tenuis (strain C-141) DNA.
FEATURES
source
1..1435
/organism="Nitrosovibrio tenuis"
/mol_type="unassigned DNA"

ORIGIN /db_xref="taxon:1233"

Query Match 100.0%; Score 19; DB 1; Length 1435;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCCCCACTCGAAGATACG 19
135 TCCCCCACTCGAAGATACG 117

RESULT 13
AP386755/c 1469 bp DNA linear ENV 10-MAY-2004
LOCUS Nitrosospira sp. R5C20 16S ribosomal RNA gene, partial sequence.
ACCESSION AP386755
VERSION AP386755.1 GI:17864832
KEYWORDS ENV.
SOURCE Nitrosospira sp. R5C20
ORGANISM Nitrosospira sp. R5C20
REFERENCE Burrell,P.C., Phalen,C.M. and Hovanec,T.A.
AUTHORS 1 (bases 1 to 1469)
TITLE Identification of bacteria responsible for ammonia oxidation in freshwater aquaria
JOURNAL Appl. Environ. Microbiol. 67 (12), 5791-5800 (2001)
PUBMED 11722936
2 (bases 1 to 1469)
AUTHORS Burrell,P.C., Phalen,C.M. and Hovanec,T.A.
TITLE Direct Submission
JOURNAL Submitted (30-MAY-2001) Aquatic Research Laboratory, The Aquaria Group, 6100 Condon Dr, Moorpark, CA 93021, USA
LOCATION/Qualifiers
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source 1. 1469
/organism="Nitrosospira sp. R5C20"
/mol_type="genomic DNA"
/isolation_source="ammonia-oxidizing bacteria isolated from freshwater aquaria enrichments"
/db_xref="taxon:180514"
/clone="R5C20"
/environmental_sample
<1. >1469
/product="16S ribosomal RNA"

ORIGIN

Query Match 100.0%; Score 19; DB 3; Length 1469;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCCCCACTCGAAGATACG 19
133 TCCCCCACTCGAAGATACG 115

RESULT 14
AF386754/c 1486 bp DNA linear ENV 10-MAY-2004
LOCUS Nitrosospira sp. BFl6c46 16S ribosomal RNA gene, partial sequence.
ACCESSION AF386754
VERSION AF386754.1 GI:17864831
KEYWORDS ENV.
SOURCE Nitrosospira sp. BFl6c46
ORGANISM Nitrosospira sp. BFl6c46
REFERENCE Burrell,P.C., Phalen,C.M. and Hovanec,T.A.
AUTHORS 1 (bases 1 to 1486)
TITLE Identification of bacteria responsible for ammonia oxidation in freshwater aquaria
JOURNAL Appl. Environ. Microbiol. 67 (12), 5791-5800 (2001)
PUBMED 11722936

REFERENCE 2 (bases 1 to 1486)
AUTHORS Burrell,P.C., Phalen,C.M. and Hovanec,T.A.
TITLE Direct Submission
JOURNAL Submitted (30-MAY-2001) Aquatic Research Laboratory, The Aquaria Group, 6100 Condon Dr, Moorpark, CA 93021, USA
LOCATION/Qualifiers
FEATURES
source 1. 1486
/organism="Nitrosospira sp. BFl6c46"
/mol_type="genomic DNA"
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/environmental_sample
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/product="16S ribosomal RNA"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 18;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCCCCACTCGAAGATACG 19
131 TCCCCCACTCGAAGATACG 113

RESULT 15
AY856079/c 1495 bp DNA linear BCT 12-JAN-2005
LOCUS Nitrosospira sp. En13 16S ribosomal RNA gene, partial sequence.
ACCESSION AY856079
VERSION AY856079.1 GI:572322110
KEYWORDS ENV.
SOURCE Nitrosospira sp. En13
ORGANISM Nitrosospira sp. En13
REFERENCE Burrell,P.C., Phalen,C.M. and Hovanec,T.A.
AUTHORS 1 (bases 1 to 1495)
TITLE Nitrosomonadaceae; Nitrosospira.
JOURNAL Nitrous oxide production and nitrifier denitrification by betaproteobacterial ammonia oxidising bacteria
AUTHORS Shaw,L.J., Nicol,G.W., Smith,Z., Fear,J., Prosser,J.I. and Baggs,E.M.
TITLE Unpublished
JOURNAL 2 (bases 1 to 1495)
REFERENCE Shaw,L.J., Nicol,G.W., Smith,Z., Fear,J., Prosser,J.I. and Baggs,E.M.
AUTHORS Direct Submission
JOURNAL Submitted (14-DEC-2004) School of Biological Sciences, University of Aberdeen, Cruickshank Building, St Machar Drive, Aberdeen AB24 3UU, U.K.
LOCATION/Qualifiers
FEATURES
source 1. 1495
/organism="Nitrosospira sp. En13"
/mol_type="genomic DNA"
/strain="En13"
/db_xref="taxon:308023"
<1. >1495
/product="16S ribosomal RNA"

ORIGIN

Query Match 100.0%; Score 19; DB 1; Length 1495;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCCCCACTCGAAGATACG 19
116 TCCCCCACTCGAAGATACG 98

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Job time : 104.614 secs

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: Apr 11 7, 2006, 08:39:29 ; Search time 2273.35 Seconds
(without alignments)
31.676 Million cell updates/sec

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Perfect score: 18
Sequence: 1 cccccctcttgatcac 18

Scoring table: Oligo NUC
Gapop 60.0, Gapext 60.0

Searched: 9267905 seqs, 2000278028 residues

Word size: 1

Total number of hits satisfying chosen parameters: 13049666

Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

Database:

Published Applications NA New:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	77.8	25	8	US-10-310-914A-1061199	Sequence 1061199,
2	77.8	25	14	US-11-121-849-112898	Sequence 112898,
3	72.2	19	12	US-11-101-244-1230837	Sequence 1230837,
4	72.2	19	13	US-11-083-784-1230837	Sequence 1230837,
5	72.2	23	8	US-10-310-914A-224598	Sequence 224598,
6	72.2	25	9	US-10-934-048A-68320	Sequence 68320, A
7	72.2	25	14	US-11-121-849-325988	Sequence 325988,
8	72.2	27	8	US-10-310-914A-224589	Sequence 224589,
9	66.7	18	8	US-10-310-914A-439308	Sequence 439308,
10	66.7	18	8	US-10-310-914A-552172	Sequence 552172,
11	66.7	19	8	US-10-310-914A-1226662	Sequence 1226662,
12	66.7	19	12	US-11-101-244-603439	Sequence 603439,
13	66.7	19	12	US-11-101-244-815438	Sequence 815438,
14	66.7	19	12	US-11-101-244-815537	Sequence 815537,
15	66.7	19	12	US-11-101-244-817168	Sequence 817168,
16	66.7	19	12	US-11-101-244-869498	Sequence 869498,
17	66.7	19	12	US-11-101-244-869507	Sequence 869507,
18	66.7	19	12	US-11-101-244-1029566	Sequence 1029566,

C 19	12	66.7	19	12	US-11-101-244-1059817	Sequence 1059817,
C 20	12	66.7	19	12	US-11-101-244-1069870	Sequence 1069870,
C 21	12	66.7	19	12	US-11-101-244-1158402	Sequence 1158402,
C 22	12	66.7	19	12	US-11-101-244-1158440	Sequence 1158440,
C 23	12	66.7	19	12	US-11-101-244-1404224	Sequence 1404224,
C 24	12	66.7	19	12	US-11-101-244-1425762	Sequence 1425762,
C 25	12	66.7	19	12	US-11-101-244-1518708	Sequence 1518708,
C 26	12	66.7	19	13	US-11-083-784-603439	Sequence 603439,
C 27	12	66.7	19	13	US-11-083-784-815438	Sequence 815438,
C 28	12	66.7	19	13	US-11-083-784-815537	Sequence 815537,
C 29	12	66.7	19	13	US-11-083-784-817168	Sequence 817168,
C 30	12	66.7	19	13	US-11-083-784-869498	Sequence 869498,
C 31	12	66.7	19	13	US-11-083-784-869507	Sequence 869507,
C 32	12	66.7	19	13	US-11-083-784-1029568	Sequence 1029568,
C 33	12	66.7	19	13	US-11-083-784-1059817	Sequence 1059817,
C 34	12	66.7	19	13	US-11-083-784-1069870	Sequence 1069870,
C 35	12	66.7	19	13	US-11-083-784-1158402	Sequence 1158402,
C 36	12	66.7	19	13	US-11-083-784-1158440	Sequence 1158440,
C 37	12	66.7	19	13	US-11-083-784-1404224	Sequence 1404224,
C 38	12	66.7	19	13	US-11-083-784-1425762	Sequence 1425762,
C 39	12	66.7	19	13	US-11-083-784-1518708	Sequence 1518708,
C 40	12	66.7	20	8	US-10-310-914A-541699	Sequence 541699,
C 41	12	66.7	20	8	US-10-310-914A-960621	Sequence 960621,
C 42	12	66.7	20	8	US-10-310-914A-1041099	Sequence 1041099,
C 43	12	66.7	21	8	US-10-310-914A-552134	Sequence 552134,
C 44	12	66.7	21	8	US-10-310-914A-596021	Sequence 596021,
C 45	12	66.7	22	8	US-10-310-914A-230052	Sequence 230052,

ALIGNMENTS

RESULT 1
US-10-310-914A-1061199/c
Sequence 1061199, Application US/10310914A
Publication No. US2006000322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310.914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1061199
LENGTH: 25
TYPE: RNA
ORGANISM: Human
US-10-310-914A-1061199

Query Match 77.8%; Score 14; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 2 CCCCCCTCTCGA 15
Db 20 CCCCCCTCTCGA 7

RESULT 2
US-11-121-849-112898
Sequence 112898, Application US/11121849
Publication No. US20050272080A1
GENERAL INFORMATION:
APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121.849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949

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; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 112898
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-112898
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Best Local Similarity 100.0%; Pred. NO. 2.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db       6  CCCCTCTGTGATA 19
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RESULT 3
US-11-101-244-1230837
; Sequence 1230837, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1230837
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1230837
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Query Match          72.2%; Score 13; DB 12; Length 19;
Best Local Similarity 61.5%; Pred. NO. 8e+02;
Matches 8; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
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Db       4  CUCUCUCGAAAC 16
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US-11-083-784-1230837
; Sequence 1230837, Application US/11083784
; Publication No. US2005024575A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
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; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1230837
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1230837
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Best Local Similarity 61.5%; Pred. NO. 8e+02;
Matches 8; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
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         |||||
Db       4  CUCUCUCGAAAC 16
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RESULT 5
US-10-310-914A-224598
; Sequence 224598, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Benwich, Isaac
; APPLICANT: Shiler, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; PRIOR FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 224598
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-224598
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Query Match          72.2%; Score 13; DB 8; Length 23;
Best Local Similarity 69.2%; Pred. NO. 8e+02;
Matches 9; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
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Db       9  CCCUCUCUGGA 21
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RESULT 6
US-10-934-048A-68320
; Sequence 68320, Application US/10934048A
; Publication No. US2006005170A1
; GENERAL INFORMATION:
; APPLICANT: Tanya Makeev
; TITLE OF INVENTION: Methods of Genetic Analysis of Yeast
; FILE REFERENCE: 3699
; CURRENT APPLICATION NUMBER: US/10/934,048A
; PRIOR FILING DATE: 2004-09-03
; NUMBER OF SEQ ID NOS: 120855
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 68320
; LENGTH: 25
; TYPE: DNA
; ORGANISM: S. pombe
US-10-934-048A-68320
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Query Match          72.2%; Score 13; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. NO. 8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      6  CTCCTCTGATAC 18
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Db       4  CTCCTCTGATAC 16
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US-11-121-849-325988
; Sequence 325988, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 325988
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-325988

Query Match      72.2%; Score 13; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      3 CCCCTCTTCTGGA 15
DB      9 CCCCTCTTCTGGA 21

RESULT 8
US-10-310-914A-224589
; Sequence 224589, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 224589
; LENGTH: 27
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-224589

Query Match      72.2%; Score 13; DB 8; Length 27;
Best Local Similarity 69.2%; Pred. No. 8e+02;
Matches 9; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY      3 CCCCTCTTCTGGA 15
DB      8 CCCCTCTTCTGGA 20

RESULT 9
US-10-310-914A-439308/c
; Sequence 439308, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
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; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 439308
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-439308

Query Match      66.7%; Score 12; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      3 CCCCTCTTCTGG 14
DB      12 CCCCTCTTCTGG 1

RESULT 10
US-10-310-914A-552172/c
; Sequence 552172, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes an
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 552172
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-552172

Query Match      66.7%; Score 12; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 CCCCTCTTCTCT 12
DB      18 CCCCTCTTCTCT 7

RESULT 11
US-10-310-914A-1226662/c
; Sequence 1226662, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1226662
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1226662

Query Match      66.7%; Score 12; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB      17 CCCCTCTTCTGG 6
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RESULT 12
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; Sequence 603439, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 603439
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-603439
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Query Match      66.7%; Score 12; DB 12; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db      18 TCTTCTGGATAC 7
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RESULT 13
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; Sequence 815438, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 815438
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-815438
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Query Match      66.7%; Score 12; DB 12; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      7 TCTTCTGGATAC 18
      |||||
Db      18 TCTTCTGGATAC 7
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RESULT 14
US-11-101-244-815537/c
; Sequence 815537, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
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; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-815537
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Query Match      66.7%; Score 12; DB 12; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      7 TCTTCTGGATAC 18
      |||||
Db      18 TCTTCTGGATAC 7
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RESULT 15
US-11-101-244-817168/c
; Sequence 817168, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 817168
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-817168
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Query Match      66.7%; Score 12; DB 12; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      7 TCTTCTGGATAC 18
      |||||
Db      18 TCTTCTGGATAC 7
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Mon Apr 10 08:45:41 2006

us-10-659-980a-5.014g_sz30.mphn

Page 5

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Job time : 2275.35 secs

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 7, 2006, 08:39:03 ; Search time 349.784 Seconds
(without alignments)
425.545 Million cell updates/sec

Title: US-10-659-980A-5

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Gapop 60.0 , Gapext 60.0

Searched: 9793542 seqs, 4134689005 residues

Word size: 3
Total number of hits satisfying chosen parameters: 10533214

Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

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Published Applications NA Main:*

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- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	18	100.0	18	US-10-659-948A-5	Sequence 5, Appl1
2	18	100.0	18	US-10-659-980A-5	Sequence 5, Appl1
3	18	100.0	18	US-10-659-983A-5	Sequence 5, Appl1
4	13	72.2	25	US-10-719-956-117959	Sequence 117959,
5	13	72.2	25	US-10-719-956-193006	Sequence 193006,
6	13	72.2	25	US-10-719-956-470164	Sequence 470164,
7	13	72.2	25	US-10-719-956-511003	Sequence 511003,
8	13	72.2	25	US-10-719-956-558629	Sequence 558629,
9	13	72.2	25	US-10-719-956-611802	Sequence 611802,
10	13	72.2	25	US-10-719-900-116050	Sequence 116050,
11	13	72.2	25	US-10-719-900-574815	Sequence 574815,
12	13	72.2	25	US-11-060-756-197597	Sequence 197597,
13	13	72.2	25	US-11-060-756-197598	Sequence 197598,
14	13	72.2	17	US-10-459-876-17	Sequence 17, Appl1
15	13	72.2	18	US-10-659-948A-6	Sequence 6, Appl1
16	13	72.2	18	US-10-659-980A-6	Sequence 6, Appl1
17	13	72.2	19	US-10-659-983A-6	Sequence 6, Appl1
18	13	72.2	18	US-10-659-983A-6	Sequence 6, Appl1
19	13	72.2	20	US-09-946-406-23	Sequence 23, Appl1
20	13	72.2	20	US-10-002-623-451	Sequence 26, Appl1
21	13	72.2	20	US-10-289-762-2493	Sequence 2493, App
22	13	72.2	20	US-10-280-183A-513	Sequence 513, App
23	13	72.2	20	US-10-684-978-26	Sequence 26, Appl1

C	24	12	66.7	25	5	US-10-215-112-6677	Sequence 6677, Ap
C	25	12	66.7	25	6	US-10-122-114-1	Sequence 1, Appl1
C	26	12	66.7	25	7	US-10-719-956-5244	Sequence 5244, Ap
C	27	12	66.7	25	7	US-10-719-956-60519	Sequence 60519, A
C	28	12	66.7	25	7	US-10-719-956-135610	Sequence 135610,
C	29	12	66.7	25	7	US-10-719-956-141395	Sequence 141395,
C	30	12	66.7	25	7	US-10-719-956-165636	Sequence 165636,
C	31	12	66.7	25	7	US-10-719-956-169435	Sequence 169435,
C	32	12	66.7	25	7	US-10-719-956-170701	Sequence 170701,
C	33	12	66.7	25	7	US-10-719-956-407739	Sequence 407739,
C	34	12	66.7	25	7	US-10-719-956-407739	Sequence 407739,
C	35	12	66.7	25	7	US-10-719-956-470165	Sequence 470165,
C	36	12	66.7	25	7	US-10-719-956-577871	Sequence 577871,
C	37	12	66.7	25	7	US-10-719-956-613937	Sequence 613937,
C	38	12	66.7	25	7	US-10-719-956-620295	Sequence 620295,
C	39	12	66.7	25	7	US-10-719-956-676929	Sequence 676929,
C	40	12	66.7	25	8	US-10-719-900-226025	Sequence 226025,
C	41	12	66.7	25	8	US-10-719-900-242303	Sequence 242303,
C	42	12	66.7	25	8	US-10-719-900-290325	Sequence 290325,
C	43	12	66.7	25	8	US-10-719-900-307739	Sequence 307739,
C	44	12	66.7	25	8	US-10-719-900-307739	Sequence 307739,
C	45	12	66.7	25	8	US-10-719-900-416880	Sequence 416880,

ALIGNMENTS

RESULT 1
US-10-659-948A-5
Sequence 5, Application US/10659948A
Publication No. US20040101946A1
GENERAL INFORMATION:
APPLICANT: Hovaneec, Timothy A
TITLE OF INVENTION: Method of Using Ammonia-Oxidizing Bacteria
FILE REFERENCE: 81289-294309
CURRENT APPLICATION NUMBER: US/10/659,948A
CURRENT FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: US 09/573,664
PRIOR FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: US 60/386,217
PRIOR FILING DATE: 2002-09-19
PRIOR APPLICATION NUMBER: US 60/386,218
PRIOR FILING DATE: 2002-09-19
PRIOR APPLICATION NUMBER: US 60/386,219
PRIOR FILING DATE: 2002-09-19
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn version 3.2
SEQ ID NO 5:
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Oligonucleotide Probe
US-10-659-948A-5
Query Match 100.0%; Score 18; DB 7; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1 cccccctctctgataac 18
1 cccccctctctgataac 18
RESULT 2
US-10-659-980A-5
Sequence 5, Application US/10659980A
Publication No. US20040106133A1
GENERAL INFORMATION:
APPLICANT: Hovaneec, Timothy A
TITLE OF INVENTION: Method for Detecting Ammonia-Oxidizing Bacteria
FILE REFERENCE: 81289-284781
CURRENT APPLICATION NUMBER: US/10/659,980A

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; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: US 09/573,684
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 60/386,217
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/386,218
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/386,219
; PRIOR FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Oligonucleotide Probe
US-10-659-980A-5

Query Match      100.0%; Score 18; DB 7; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCCCCCTCTCGATAC 18
DB      1 CCCCCCTCTCTGGATAC 18

RESULT 3
US-10-659-983A-5
; Sequence 5, Application US/10659983A
; Publication No. US2004015731A1
; GENERAL INFORMATION:
; APPLICANT: Hovaneec, Timothy A
; TITLE OF INVENTION: Ammonia-Oxidizing Bacteria
; FILE REFERENCE: 81289-284779
; CURRENT APPLICATION NUMBER: US/10/659,983A
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: US 09/573,684
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 60/386,217
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/386,218
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/386,219
; PRIOR FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Oligonucleotide Probe
US-10-659-983A-5

Query Match      100.0%; Score 18; DB 7; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCCCCCTCTCTCGATAC 18
DB      1 CCCCCCTCTCTGGATAC 18

RESULT 4
US-10-719-956-117959/c
; Sequence 117959, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; FILE REFERENCE: 3527.1
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; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 117959
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-117959

Query Match      72.2%; Score 13; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 CTCTCTCGATAC 18
DB      19 CTCTCTCGATAC 7

RESULT 5
US-10-719-956-193006
; Sequence 193006, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 193006
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-193006

Query Match      72.2%; Score 13; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 CCCTCTCTCGAT 16
DB      4 CCCTCTCTCGAT 16

RESULT 6
US-10-719-956-470164
; Sequence 470164, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 470164
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-470164

Query Match      72.2%; Score 13; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 5 CCTCTCTGGATA 17
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Db 13 CCTCTCTGGATA 25

RESULT 7
US-10-719-956-511003
; Sequence 511003, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002.11.20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 511003
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-511003

Query Match 72.2%; Score 13; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 CCTCTCTGGAT 16
| | | | | | | | | |
Db 10 CCTCTCTGGAT 22

RESULT 8
US-10-719-956-558629
; Sequence 558629, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002.11.20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 558629
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-558629

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Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 CCTCTCTGGAT 16
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Db 7 CCTCTCTGGAT 19

RESULT 9
US-10-719-956-611802
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; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956

; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002.11.20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 611802
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-611802

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Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 CCTCTCTGGA 15
| | | | | | | | | |
Db 6 CCTCTCTGGA 18

RESULT 10
US-10-719-900-316050
; Sequence 316050, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002.11.20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 316050
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-316050

Query Match 72.2%; Score 13; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 CCTCTCTGGATA 17
| | | | | | | | | |
Db 4 CCTCTCTGGATA 16

RESULT 11
US-10-719-900-574815
; Sequence 574815, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002.11.20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 574815
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-574815

Query Match 72.2%; Score 13; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CTCCTCTTGATAC 18
|||
Db 7 CTCCTCTTGATAC 19

RESULT 12

US-11-060-756-197597/c
; Sequence 197597, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mount, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 197597
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-197597

Query Match 72.2%; Score 13; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCCTCTTGGA 15
|||
Db 18 CCCCTCTTGGA 6

RESULT 13

US-11-060-756-197598/c
; Sequence 197598, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mount, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 197598
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-197598

Query Match 72.2%; Score 13; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCCTCTTGGA 15
|||
Db 18 CCCCTCTTGGA 6

RESULT 14

US-10-459-876-17
; Sequence 17, Application US/10459876
; Publication No. US20030208060A1
; GENERAL INFORMATION:
; APPLICANT: Glanturco, S.H.
; APPLICANT: Bradley, W.A.
; TITLE OF INVENTION: DNA Encoding Human apob48R: A Monocyte-Macrophage
; TITLE OF INVENTION: Apolipoprotein B48 Receptor Gene and Protein
; FILE REFERENCE: D5880CIP

; CURRENT APPLICATION NUMBER: US/10/459,876
; CURRENT FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: US/09/583,610
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: US 09/130,242
; PRIOR FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 22
; SEQ ID NO 17
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense primers were based on the 5'-end
; OTHER INFORMATION: sequence of the THP-1 (73 clone) (bp 2203-2187
US-10-459-876-17

Query Match 66.7%; Score 12; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCTCTCTTGAT 16
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Db 5 CCTCTCTTGAT 16

RESULT 15

US-10-659-948A-6/c
; Sequence 6, Application US/10659948A
; Publication No. US20040101946A1
; GENERAL INFORMATION:
; APPLICANT: Hovane, Timothy A
; TITLE OF INVENTION: Method of Using Ammonia-Oxidizing Bacteria
; FILE REFERENCE: 81289-294309
; CURRENT APPLICATION NUMBER: US/10/659,948A
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: US 09/573,684
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 60/386,217
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/386,218
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/386,219
; PRIOR FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: PCR Primer
US-10-659-948A-6

Query Match 66.7%; Score 12; DB 7; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 TCTTCTGATAC 18
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Db 18 TCTTCTGATAC 7

Search completed: April 7, 2006, 09:17:27
Job time : 350.784 secs